FIGURE 1

Human DNase I

```
LOCUS
            HUMDNASEI
                         1039 bp
                                    mRNA
                                                     PRI
                                                               06-MAR-1995
DEFINITION
            Human DNase I mRNA, complete cds.
ACCESSION
            M55983
            M55983.1 GI:181623
VERSION
KEYWORDS
            DNase I.
SOURCE
            Human pancreus, cDNA to mRNA.
  ORGANISM
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
               (bases 1 to 1039)
  AUTHORS
            Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
            Recombinant human DNase I reduces the viscosity of cystic fibrosis
  TITLE
            sputum
  JOURNAL
            Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
  MEDLINE
            91067672
FEATURES
                     Location/Qualifiers
     source
                     1..1039
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                     /db xref="taxon:9606"
                     /clone="hDNase-18-1"
                     /tissue_type="pancreas"
     sig peptide
                     160..225
                     /gene="DNase I"
     CDS
                     160..1008
                     /gene="DNase I"
                     /codon start=1
                     /product="DNase I"
                     /protein id="AAA63170.1"
                     /db xref="GI:181624"
                     /translation="MRGMKLLGALLALAALLQGAVSLKIAAFNIQTFGETKMSNATLV
                     SYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNQDAPDTYHYVVSEPLGRNSYKERY
                     LFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFSRFTEVREFAIVPLHAAPG
                     DAVAEIDALYDVYLDVQEKWGLEDVMLMGDFNAGCSYVRPSQWSSIRLWTSPTFQWLI
                     {\tt PDSADTTATPTHCAYDRIVVAGMLLRGAVVPDSALPFNFQAAYGLSDQLAQAISDHYP}
                     VEVMLK"
     gene
                     160..1008
                     /gene="DNase I"
     mat peptide
                     226..1005
                     /gene="DNase I"
                     /product="DNase I"
BASE COUNT
                         305 с
                226 a
                                  282 q
                                            226 t
ORIGIN
        1 tcctgcacag gcagtgcctt gaagtgcttc ttcagagacc tttcttcata gactactttt
       61 ttttctttaa gcagcaaaag gagaaaattg tcatcaaagg atattccaga ttcttgacag
      121 cattetegte atetetgagg acateaceat cateteagga tgaggggeat gaagetgetg
      181 ggggcgctgc tggcactggc ggccctactg cagggggccg tgtccctgaa gatcgcagcc
      241 ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt
      301 gtgcagatcc tgagccgcta tgacatcgcc ctggtccagg aggtcagaga cagccacctg
      361 actgccgtgg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac
      421 gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg
      481 cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgcga gccctgcggg
      541 aacgacacet teaacegaga gecageeatt gteaggttet teteeeggtt caeagaggte
      601 agggagtttg ccattgttcc cctgcatgcg gccccggggg acgcagtagc cgagatcgac
      661 gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttggagga cgtcatgttg
      721 atgggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtggtc atccatccgc
      781 ctgtggacaa geeceaectt ccagtggetg ateceegaca gegetgacae cacagetaca
      841 cccacgcact gtgcctatga caggatcgtg gttgcaggga tgctgctccg aggcgccgtt
      901 gittesegact eggetettee etttaaette eaggetgeet atggeetgag tgaccaactg
      961 gcccaagcca tcagtgacca ctatccagtg gaggtgatgc tgaagtgagc agcccctccc
     1021 cacaccagtt gaactgcag
11
```

FIGURE 2

```
LOCUS
               MHDNASE.DN
                                 783 bp
                                             mPNA
                                                                 PRI
                                                                               06-MAR-1995
               Human DNase I mRNA, complete cds, Mature sequence modified to remove Narl site
DEFINITION
ACCESSION
               M55983
NID
               g181623
KEYWORDS
               DNase I.
SOURCE
               Human pancreus, cDNA to mRNA.
  ORGANISM
               Homo sapiens
               Eukaryotae; mitochondrial eukaryotea; Metazoa; Chordata;
               Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Komo.
REFERENCE
                   (bases 1 to 1039)
  AUTHORS
               Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
               Recombinant human DNase I reduces the viscosity of cystic fibrosis
  TITLE
               Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
  JOURNAL
  MEDLINE
               91067672
FEATURES
                          Location/Qualifiers
      source
                           1. .1039
                           /organism="Homo sapiens"
                           /db_xref="taxon:9606"
                           /clone="hDNase-18-1"
                          /tissue_type="pancreas"
160. .225
      sig_peptide
                           /gene="DNase I"
      CDS
                           160. .1008
                           /gene≃"DNase I"
                           /codon_start=1
                           /product="DNase I"
                           /db_xref "FID:g181624"
                           translation="LKIAAFNIQTFGETKMSNATLVSYIVQILSRYDIALVQEVRDSH"
                           LTAVGKLLDNLNQDAPDTYHYVVSEPLGRNSYKERYLFVYRPDQVSAVDSYYYDDGCE
                           PCGNDTFNREPAIVRFFSRFTEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKKGL
                           EDVMLMGDFNAGCSYVRPSQWSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAG
                           MLLRGAVVFDSALEFNFQAAYGLSDQLAQAISDHYPVEVMT.K*
      gene
                           160. .1008
                           /gene="DNase I"
                           226. .1005
      mat_peptide
                           /gene="DNase I"
                           /product="DNase I"
BASE COUNT
                    168 a
                               236 c
                                          220 g
                                                      159 t.
ORIGIN
       1 CIGAMGATCG CAGCCTICAA CATCCAGACA TITGGGGAGA CCAAGATGTC CAATGCCACC 61 CICGICAGCI ACATIGIGCA GATCCTGAGC CGCTACGACA TCGCCCIGGT CCAGGAGGTC 121 AGAGACAGCC ACCIGACTGC CCTGGGGAAC CIGCTGGACA ACCTCAATCA GGACGCACCA
        181 GACACCTATC ACTACGTGGT CAGTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC
        241 CIGTICGIGT ACAGGCCTGA CCAGGTGTCT GCGGTGGACA GCTACTACTA CGATGAIGGC
        301 TGCGAGCCCT GCGGGAACGA CACCTTCAAC CGAGAGCCAG CCATTGTCAG GTTCTTCTCC
       361 CCGTTCACAG AGGTCAGGGA GITIGCCATI GTTCCCCTGC ATGCGGCCCC GGGGGACGCA
421 GTAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
       481 GAGGACGICA IGITGATGGG CGACTICAAT GGGGGGTGGA GCTATGTGAG ACCCTCCAG
541 TGGTCATCCA ICCGCCTGTG GACAAGCCC ACCTICCAGT GGCTGATCCC CGACAGCGCT
601 GACACCACAG CTACACCCAC GCACTGTGC TAIGACAGGA TCGTGGTTGC AGGGATGCTG
661 CICCGAGGGG CCGTTGTTCC CGACTCGGCT CTTCCCTTTA ACTTCCAGGC TGCCTATGGC
        721 CIGAGIGACC AACIGGCCCA AGCCATCAGI GACCACIAIC CAGIGGAGGI GAIGCIGAAG
        781 TGA
```

į.

FIGURE 2(B)

```
SYN
                                                               29-AUG-2000
                          858 BP SS-DNA
LOCUS
            PAS155 GB.
DEFINITION
ACCESSION
KEYWORDS
SOURCE
                     Location/Qualifiers
FEATURES
                     10..75
     frag
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                     <10..>75
     frag
                     /note="1 to 1039 of M55983.DNA [Split]"
     source
                     /organism="Homo sapiens"
                     /db xref="taxon:9606"
                     /clone="hDNase-18-1"
                     /tissue_type="pancreas [Split]"
                     10..75
     sig peptide
                      /gene="DNase I"
                      10..>75
     CDS
                      /gene="DNase I"
                      /codon start="1"
                      /product="DNase I"
                      /db_xref="PID:g181624"
                      translation="MRGMKLLGALLALAALLQGAVS|LKIAAFNIQTFGETKMSNATLV/
                      SYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNQDAPDTYHYVVSEPLGRNSYKERY
                      LFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFSRFTEVREFAIVPLHAAPG
                      D... [Split]"
                      10..>75
     gene
                      /gene="DNase I [Split]"
     fraq
                      /note="1 to 783 of mod humanDNAseI"
                      76..858
      fraq
                      /note="1 to 72 of 104linker"
                      join(76..>129,<131..147)
      frag
                      /note="1 to 72 of 103linker [Split]"
                      join(76..>126,<127..>129,<131..147)
      frag
                      /note="1 to 78 of 102linker [Split]"
                                             170 T
                                                        0 OTHER
 ANSE COUNT
                                   251 G
                 177 A
                          260 C
 ORIGIN
         1 GCCGCCACCA TGAGGGGCAT GAAGCTGCTG GGGGCGCTGC TGGCACTGGC GGCCCTACTG
        61 CAGGGGGCCG TGTCCCTGAA GATCGCAGCC TTCAACATCC AGACATTTGG GGAGACCAAG
       121 ATGTCCAATG CCACCCTCGT CAGCTACATT GTGCAGATCC TGAGCCGCTA CGACATCGCC
       181 CTGGTCCAGG AGGTCAGAGA CAGCCACCTG ACTGCCGTGG GGAAGCTGCT GGACAACCTC
       241 AATCAGGACG CACCAGACAC CTATCACTAC GTGGTCAGTG AGCCACTGGG ACGGAACAGC
       301 TATAAGGAGC GCTACCTGTT CGTGTACAGG CCTGACCAGG TGTCTGCGGT GGACAGCTAC
       361 TACTACGATG ATGGCTGCGA GCCCTGCGGG AACGACACCT TCAACCGAGA GCCAGCCATT
       421 GTCAGGTTCT TCTCCCGGTT CACAGAGGTC AGGGAGTTTG CCATTGTTCC CCTGCATGCG
       481 GCCCCGGGGG ACGCAGTAGC CGAGATCGAC GCTCTCTATG ACGTCTACCT GGATGTCCAA
       541 GAGAAATGGG GCTTGGAGGA CGTCATGTTG ATGGGCGACT TCAATGCGGG CTGCAGCTAT
       601 GTGAGACCCT CCCAGTGGTC ATCCATCCGC CTGTGGACAA GCCCCACCTT CCAGTGGCTG
       661 ATCCCCGACA GCGCTGACAC CACAGCTACA CCCACGCACT GTGCCTATGA CAGGATCGTG
       721 GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT GTTCCCGACT CGGCTCTTCC CTTTAACTTC
       781 CAGGCTGCCT ATGGCCTGAG TGACCAACTG GCCCAAGCCA TCAGTGACCA CTATCCAGTG
```

841 GAGGTGATGC TGAAGTGA

(A) pAS6 - light chain

```
LOCUS
              HMFGllC2.D
                                721 bp
                                              DNA
DEFINITION HUMANISED HMFG1 LIGHT CHAIN VOD LEADER.
ACCESSION . .
KEYWORDS
SOURCE
  ORGANISM
               1 (BASES 1 TO 342)
VERHOEYEN ET AL
CONSTRUCTION OF RESHAPED HMFG1 ETC
IMMUNOL. (1993):78, 364-370
REFERENCE
  AUTHORS
  TITLE
   JOURNAL
COMMENT
               SCANNED IN FROM JOURNAL
FEATURES
  SITES
```

This is the sequence of the HMFG1 light chain gene with the Vnp leader sequence attached. Translate from residue 1. Note residue 399 is T > A in all clones leading to Rl33 silent mutation (T in Verhoeyen paper)

BASE COUNT 197 a 202 c 162 g 140 t
ORIGIN 7 | FADEA SEA

٧		venver	OEQ			
`1	ATGGGATGGA	GCTGTATCAT	CCTCTTCTTG	GTAGCAACAG	CTACAGGTGT	CCACTCCGAC
61	ATCCAGATGA	CCCAGAGCCC	AAGCAGCCTG	AGCGCCAGCG	TGGGTGACAG	AGTGACCATC
121	ACCTGTAAGT	CCAGTCAGAG	CCTTTTATAT	AGTAGCAATC	AAAAGATCTA	CTTGGCCTGG
181	TACCAGCAGA	AGCCAGGTAA	GGCTCCAAAG	CTGCTGATCT	ACTGGGGATC	CACTAGGGAA
241	TCTGGTGTGC	CANGCAGATT	CAGCGGTAGC	GGTAGCGGTA	CCGACTTCAC	CTTCACCATC
301	AGCAGCCTCC	AGCCAGACGA	CATCGCCACC	TACTACTGCC	AGCAATATTA	ፕ ልGგ ፕልፕሮሮጥ
361	CEGACGTTCG	GCCAAGGGAC	CAAGGTGGAA	ATCAAACGAA	CTGTGGCTGC	ACCATCTGTC
421	TICATCTICC	CGCCATCTGA	TGAGCAGTIG	AAATCTGGAA	CTGCCTCTGT	TGTGTGCCTG
481	CIGAATAACI	TCTATCCCAG	AGAGGCCAAA	GTACAGTGGA	AGGTGGATAA	CGCCCTCCAA
541	ICGGGTAACT	CCCAGGAGAG	TGTCACAGAG	CAGGACAGCA	AGGACAGCAC	CTACAGCCTC
601	AGCAGCACCC	TGACGCTGAG	CAAAGCAGAC	TACGAGAAAC	ACAAAGTCTA	CGCCTGCGAA
661	GTCACCCATC	AGGGCCTGAG	CTCGCCCGTC	ACAAAGAGCT	TCAACAGGGG	AGAGTGTTAG
721	λ					

//

Figure 3(B)

```
29-AUG-2000
                         730 BP SS-DNA
                                                    SYN
           HHMFG1KLC
LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
                    Location/Qualifiers
FEATURES
                     10..730
     frag
                     /note="1 to 721 of hHMFGllight chain"
                     10..730
     frag
                     /note="1 to 72 of 104linker"
     frag
                     join(10..>63,<65..81)
                     /note="1 to 72 of 103linker [Split]"
                     join(10..>60,<61..>63,<65..81)
     frag
                     /note="1 to 78 of 102linker [Split]"
"SE COUNT
                         208 C
                                 184 G
                                           140 T
                                                      0 OTHER
                198 A
FIGIN
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCGACA TCCAGATGAC CCAGAGCCCA AGCAGCCTGA GCGCCAGCGT GGGTGACAGA
      121 GTGACCATCA CCTGTAAGTC CAGTCAGAGC CTTTTATATA GTAGCAATCA AAAGATCTAC
      181 TTGGCCTGGT ACCAGCAGAA GCCAGGTAAG GCTCCAAAGC TGCTGATCTA CTGGGCATCC
      241 ACTAGGGAAT CTGGTGTGCC AAGCAGATTC AGCGGTAGCG GTAGCGGTAC CGACTTCACC
      301 TTCACCATCA GCAGCCTCCA GCCAGAGGAC ATCGCCACCT ACTACTGCCA GCAATATTAT
      361 AGATATCCTC GGACGTTCGG CCAAGGGACC AAGGTGGAAA TCAAACGAAC TGTGGCTGCA
      421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCCTCTGTT
      481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
      541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
      601 TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
      661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
      721 GAGTGTTAGA
```

Figure 3 (c)

HMFG-1 light chain with Vnp Leader (shaded)

MGWSCILFLVATATGVHSDIQMTQSPSSLSASVGDRVTITCKSSQSL LYSSNQKIYLAWYQQKPGKAPKLLIYWASTRESGVPSRFSGSGSGT DFTFTISSLQPEDIATYYCQQYYRYPRTFGQGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV TEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC

(0) PAS6 - heavy drain

```
HHMFG1HC.D
                                     1404 bp
DEFINITION HUMANISED HMFG1 heavy chain
ACCESSION HHMEGIN
KEYWORDS
SOURCE
   ORGANISM
REFERENCE
                  VERHOEYEN ET AL
   AUTHORS
   TITLE
                  CONSTRUCTION OF RESHAPED HMFG1 etc
                  IMMUNOL. (1993):78, 364-370
   JOURNAL
COMMENT
                  VH domain SCANNED IN FROM JOURNAL
                  AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES
                  Residue 963 is G > T leading to silent mutation in all clones
FEATURES
   SITES
BASE COUNT
                        333 a
                                     439 c
                                                  379 g
                                                               253 t
ORIGIN
                                               LEAPER .
          1 ATGGGATEGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
         121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
         301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGGG
481 GCCCTGGGT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
541 GGCGCCTGA CCAGCGGGGT GCACACCTTC CCGGACCGG TGACGGTGTC GAGGACTCTAC
601 TCCCTCAGCA GCGGGGTAC CGTGCCCTCC AGCACCTTGG GCACCCAGAC CTACATCTGC
         661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAAACTC ACAAGTGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCC TGAGGTCACA
841 TGCGTGGTGG TGGACGTGAG CACCGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
         901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
         961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
       1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
       1081 GGGCAGCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
        1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
        1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
        1381 CTCTCCCTGT CTCCGGGTAA ATGA
                                                  * ANTIGODY DWINE FUSIONS Made MERE (34-39.)
11
             End of lower hingergion of HEAVY CHAIN. PAPE
                   Ado SEQ. Fab', Fusions were Made at the point.
                  Those with HYBRID HINGES ARE MIERED PORTHER
           THIS PART GACAAAACTGACACA
```

AFTER THIS SEQUENCE YOUGET THE
MYBRID HINGE & CINKER SEQUENCES
Than DriAze I (eg Fab-DNase construct pAS302)

Constru	Constructs pAS34/37
AS80	GAG AGG GAC AGA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC L S L S P G K G S G G L K I A A F N HMFL-I LINKEA
Constru	Constructs pAS35/38
AS81 AS82 (Construction	AS81 GAG AGG GAC AGA GGG AGC GGG GTG AAG ATC GCA GCC TTC AAC AS82 GAG AGG GAC AGA GGC $\frac{1}{2}$
AS83 AS84 Oligos i	AS83 AS84 GAG AGG GAC AGA GGG CCC CGG CCC AAG ATC GCA GCC TTC AAC AS84 GAG GAC AGA GGG CCC CGG CCC GAC TTC TAG L S L S P $/ / / / / / / / / / / / / / / / / / /$

AS73 AS74

To All the first that the first outs that the first the first that the first that

(A) pAS23

1554 bp mRNA PRI PAS23.DNA Humanised HMFG1 Fab'2 fused to human DNase I (construct 1) DEFINITION ACCESSION NTD **KEYWORDS** DNase I. DNase I sequence is from assembled oligos (thus modified c/f SOURCE MHDNASE1.dna) Homo sapiens ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L. AUTHORS Recombinant human DNase I reduces the viscosity of cystic fibrosis TITLE Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990) **JOURNAL** 91067672 MEDLINE 308 t 344 a 468 c 434 g BASE COUNT ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAG GGAGCGGCGG GCTGAAGATC 781 GCAGCCTTCA ACATCCAGAC ATTTGGGGAG ACCAAGATGT CCAATGCCAC CCTCGTCAGC 841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC 901 CACCTGACTG CCGTGGGGAA GCTGCTGGAC AACCTCAATC AGGACGCACC AGACACCTAT 961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTCGTG 1021 TACAGGCCTG ACCAGGTGTC TGCGGTGGAC AGCTACTACT ACGATGATGG CTGCGAGCCC 1081 TGCGGGAACG ACACCTTCAA CCGAGAGCCA GCCATTGTCA GGTTCTTCTC CCGGTTCACA 1141 GAGGTCAGGG AGTTTGCCAT TGTTCCCCTG CATGCGGCCC CGGGGGACGC AGTAGCCGAG 1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGGCTT GGAGGACGTC 1261 ATGTTGATGG GCGACTTCAA TGCGGGCTGC AGCTATGTGA GACCCTCCCA GTGGTCATCC 1321 ATCCGCCTGT GGACAAGCCC CACCTTCCAG TGGCTGATCC CCGACAGCGC TGACACCACA 1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGGTTG CAGGGATGCT GCTCCGAGGG 1441 GCCGTTGTTC CCGACTCGGC TCTTCCCTTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC 1501 CAACTGGCCC AAGCCATCAG TGACCACTAT CCAGTGGAGG TGATGCTGAA GTGA

//

Figure 5 (B)

```
25-AUG-2000
                         1554 BP SS-DNA
                                                    SYN
            FDDNASE23
LOCUS
DEFINITION
* CCESSION
 ...YWORDS
°∩URC 3
                     Location/Qualifiers
ATURES
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                     /note="1 to 1554 of 23.dna [Split]"
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     frag
                     /note="1 to 66 of 23/27linker"
                     join(721..>735,<736..786)
     frag
                     /note="1 to 78 of 102linker [Split]"
                                  435 G
                                           309 T
                         466 C
BASE COUNT
                344 A
ORIGIN
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       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
     , 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
     . 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
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      901 CACCTGACTG CCGTGGGGAA GCTGCTGGAC AACCTCAATC AGGACGCACC AGACACCTAT
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      1441 GCCGTTGTTC CCGACTCGGC TCTTCCCTTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC
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Figure S (c)

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            FDDNASE23K
DEFINITION
CCESSION
* YWORDS
SOURCE
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                         472 C
                                  437 G
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       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
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      181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
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1 .
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
in
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
j \in \mathcal{V}
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG GAGCGGCGGG
      781 CTGAAGATCG CAGCCTTCAA CATCCAGACA TTTGGGGAGA CCAAGATGTC CAATGCCACC
      841 CTCGTCAGCT ACATTGTGCA GATCCTGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGTC
      901 AGAGACAGCC ACCTGACTGC CGTGGGGAAG CTGCTGGACA ACCTCAATCA GGACGCACCA
      961 GACACCTATC ACTACGTGGT CAGTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC
     1021 CTGTTCGTGT ACAGGCCTGA CCAGGTGTCT GCGGTGGACA GCTACTACTA CGATGATGGC
     1081 TGCGAGCCCT GCGGGAACGA CACCTTCAAC CGAGAGCCAG CCATTGTCAG GTTCTTCTCC
     1141 CGGTTCACAG AGGTCAGGGA GTTTGCCATT GTTCCCCTGC ATGCGGCCCC GGGGGACGCA
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File: PAS23.DNA Range: 1 - 1554 Mode: Normal FIGURE S(D)

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-] -

CTC	TAC	603 TCC		AGC	612 AGC (GTG		GTG	CCC	630 TCC	AGC		639 TTG	GGC		648 CAG
 L	 Y	 S		 S	 S	v	 V	т	 V	 P	 S	 S	 S	 L	 G	 T	Q
ACC					666 GTG												
Т	Y	Ι	С	N	V			K			N 738	Т	K	V 747	D	К	К 756
GTT	GAG	711 CCC	AAA	TCT	720 TGT		AAA								CCA	GCA	
v	E	P	K	s	С	D	K	T	Н	Т	С	P	P	С	P	A	P
GAA	GGG	765 AGC	GGC	GGG	774 CTG			783 GCA		TTC		ATC	CAG	801 ACA	TTT	GGG	810 GAG
E	G	s	G	G	L	K	I	A	A	F	N	I	Q	T	F	G	Е
ACC	AAG	819 ATG		TAA	828 GCC	ACC	CTC	837 GTC		TAC	846 ATT		CAG	855 ATC		AGC	864 CGC
 T	K	M	S	N	Α	т	L	V	S	Y		V	Q	I	L	S	R
TAC	GAC	873 ATC		CTG	882 GTC		GAG			. GAC	-		CTG			: GTG	
Υ	D	. .	A	L	V	Q	E	V	R	D	S	Н	L	Т	Α	V	G
DAA	CTO	92° G CT		C AAC	936 CTC		CAC	-		A CCA			rat :	963 CAC		GTC	972 G GTC
K	L	L	D	N	L	N	Q	D	A	P	D	Т	Y	Н	Y	V	V
AG	r ga	98 G CC		G GG/	990 A CGG		: AG			G GA			CTC			G TAC	1026 C AGG
S	E	 P	 L	G	R	N	s	Y	K	E	R	Y	L	F	V	Y	R
CC'	T GA	103 C CA		G TC	1044 T GCC	GT	G GA	C AG	C TA	C TA	C TA	C GA	T GA	T GG		C GA	1080 G CCC
 P	 D		 ! V														Р
TG	C GG	108 G A#	-	C AC		C AA	c cg	A GA	G CC	A GC		T GT		G TT	С ТТ		1134 C CGG
C	(1 2	J D														R
ТТ		CA GA	AG G1	C AG	G GA	G TT	T GC	C AT	T GT	T CC	CC CI	G CA	T GC	G GC	C CC	G GG	1188 G GAC
F																	G D
		11	9 7		120	6		121	.5		122	2.4		123	33		1242

GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA A V A E I D A L Y D V Y L D V Q E K 1251 1260 1269 1278 1287 1296 TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT $\hbox{\tt W} \quad \hbox{\tt G} \quad \hbox{\tt L} \quad \hbox{\tt E} \quad \hbox{\tt D} \quad \hbox{\tt V} \quad \hbox{\tt M} \quad \hbox{\tt L} \quad \hbox{\tt M} \quad \hbox{\tt G} \quad \hbox{\tt D} \quad \hbox{\tt F} \quad \hbox{\tt N} \quad \hbox{\tt A} \quad \hbox{\tt G} \quad \hbox{\tt C} \quad \hbox{\tt S} \quad \hbox{\tt Y}$ 1305 1314 1323 1332 1341 1350 GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG ___ ___ V R P S Q W S S I R L W T S P T F Q 1359 1368 1377 1386 1395 1404 TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---1413 1422 1431 1440 1449 1458 GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG --- --- --- --- --- --- --- --- --- --- --- --- ---1467 1476 1485 1494 1503 1512 GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA ___ ___ ___ 1521 1530 1539 1548 GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3' A I S D H Y P V E V M L K *

(h) pAS27

PRI 06-MAR-1995 1584 bp LOCUS DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40 NLS(construct ACCESSION NID DNase I. KEYWORDS DNase I sequence is from assembled oligos (thus modified c/f SOURCE MHDNASE1.dna) ORGANISM Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L. **AUTHORS** Recombinant human DNase I reduces the viscosity of cystic fibrosis TITLE sputum Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990) JOURNAL MEDLINE 91067672 474 c 446 g 310 t BASE COUNT 354 aORIGIN 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG

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LA NLS

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DEFINITION
ACCESSION
KEYWORDS
COURCE
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     1561 CCCAAAAGA AGCGCAAGGT TTGA
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Figure 6(c)

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           FDDNASE27K
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DEFINITION
ACCESSION
KEYWORDS
SOURCE
                     Location/Qualifiers
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                                  449 G
                         478 C
BASE COUNT
CRIGIN
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DE
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      721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG GAGCGGCGGG
      781 CTGAAGATCG CAGCCTTCAA CATCCAGACA TTTGGGGAGA CCAAGATGTC CAATGCCACC
      841 CTCGTCAGCT ACATTGTGCA GATCCTGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGTC
      901 AGAGACAGCC ACCTGACTGC CGTGGGGAAG CTGCTGGACA ACCTCAATCA GGACGCACCA
      961 GACACCTATC ACTACGTGGT CAGTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC
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     1201 GTAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
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5'

File: PAS27.DNA
Range: 1 - 1584 Mode: Normal
Codon Table: Universal

FIGURE 6(D)

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																	~
М	G	W	S	С	I	Ι	L	F	L	V	A	T	A	Т	G	V	Н
		63			72			81			90			99			108
TCC	CAG		CAG	CTG		CAG	TCT		GCA	GAG	GTG	AAA	AAG		GGG	GCC	
	~									~					-~-		
S	Q	V	Q	\mathbf{L}	V	Q	S	G	A	E	V	K	K	P	G	A	S
		117			126			125			144			153			163
GTG	AAG	117 GTG	TCC	TGC	126 AAG	GCT	тст	135 GGC	TAC	ACC	144 TTC	AGT	GCC		TGG	АТА	
																	~
V	K	V	s	C	K	Α	S	G	Y	T	F	s	A	Y	W	1	E
maa	oma	171	616	aam.	180	CO 2		189	ama	a. a	198	ama	gg.	207	3.000	mm s	21
166			CAG	GC1			AAG			GAG	TGG		GGA	GAG	ATT		
W	V	R	Q	A	P	G	K	G	L	E	W	v	G	E	I	L	P
CCA	ልርጥ	225 225	ጥፈል	ጥጉጥ	234	ጥልሮ	ጥልል	243 GAG	DAG	ጥጥር	252 AAG	GGC	CGA	261 crc	۵۵۵	GTC	27
								~						~			
G	S	N	N	s	R	Y	N	E	K	F	K	G	R	V	T	V	Т
ארא	CAC	279		א כי א	288		CCC	297		CAC	306 CTC	እርር	NCC.	315	NCC.	TOT.	32
					~~-						~						
R	D	T	S	\mathbf{T}	N	\mathbf{T}	Α	Y	M	E	L	S	S	L	R	S	E
					2.40			251			2.50			2.60			
CAC	מרמ	333		ጥልጥ	342		CCA	351		ጥልር	360 GAC		GCC	369		CCT	37 מיחי
D	T	Α	V	Y	Y	С	А	R	S	Y	D	F	A	W	F	A	Y
TCC		387		ነ አርጥ	396		י אריא	405		ጥር አ	414		200	423		CCA	43
166		CAA		ACI			ACA			1 C F	GCC			AAC			
W	G	Q	G	\mathbf{T}	L	V	\mathbf{T}	V	S	S	Α	S	\mathbf{T}	K	G	q	5
CmC	n mmc	441			450		· moo			·				477			48
	. 110			- GCP			. 100	. AAG	AGC	. ACC	TCT			. ACF			. (1
V	F	P	L	A	P	S	S	K	S	Т	S	G	G	\mathbf{T}	А	A	I
COC	n ma	499			504					000	366			531			54
		. CTC		: AAC		. TAC					G GTC					- AAC	
	С	L	V								V			S		N	:
G	~																
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603 639 621 630 612 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG L Y S L S S V V T V P S S S L G T Q 693 675 684 666 657 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA T Y I C N V N H K P S N T K V D K 747 738 711 720 729 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT ___ ___ 783 792 801 774 765 GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG 855 846 837 828 ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC $\begin{smallmatrix} T & & K & & M & & S & & N & & A & & T & & L & & V & & S & & Y & & I & & V & & Q & & I & & L & & S & & R \\ \end{smallmatrix}$ 909 891 900 882 873 TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG --- --- --- --- --- --- --- --- --- --- --- --- ---927 936 945 954 963 AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC --- --- --- --- --- --- --- --- --- --- --- ---K L L D N L N Q D A P D T Y H Y V 999 1008 1017 1026 990 AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG E P L G R N S Y K E R Y L F V Y R 1044 1053 1062 1071 1035 CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC P D Q V S A V D S Y Y Y D D G C E P 1089 1098 1107 1116 1125 1134 TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG C G N D T F N R E P A I V R F F S R 1179 1188 1152 1161 1170 1143 TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC 1224 1233 1242 1197 1206 1215

GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA --- --- --- --- --- --- --- --- --- --- --- --- --- ---A V A E I D A L Y D V Y L D V Q E K 1251 1260 1269 1278 1287 1296 TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT 1305 1314 1323 1332 1341 GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG V R P S Q W S S I R L W T S P T F Q 1359 1368 1377 1386 1395 1404 TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT --- --- --- --- --- --- --- --- --- --- --- --- ---W L I P D S A D T T A T P T H C A Y 1413 1422 1431 1440 1449 GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG --- --- --- --- --- --- --- --- --- --- --- ---1476 1485 1494 1503 1512 GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA 1521 1530 1539 1548 1557 1566 GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA --- --- --- --- --- --- --- --- --- --- --- --- ---A I S D H Y P V E V M L K G G G P

1575 1584

AAG AAG CGC AAG GTT TGA 3'

K K R K V *

(A) pAS34

2196 bp 2196 bp DNA 14-AUG-1998 LOCUS PAS34.DNA 2196 bp HUMANISED HMFG1 heavy chain fused to human DNAse construct 34 DEFINITION Clone 16.4.2 (same as hcdnasel.dna template file) DEFINITION REFERENCE VERHOEYEN ET AL **AUTHORS** CONSTRUCTION OF RESHAPED HMFG1 etc TITLE IMMUNOL. (1993):78, 364-370 **JOURNAL** Human DNAse sequence is modified as a result of oligo assembly COMMENT (mhdnase.dna) The fusion was made using overlapping oligos AS79 and AS80 COMMENT AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A) **FEATURES** Residue 963 is G > T leading to silent mutation in all clones **FEATURES** SITES 501 a 677 c 607 q 411 t BASE COUNT ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG 1021 TGCAAGGTCT CCAACAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG 1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 1381 CTCTCCCTGT CTCCGGGTAA A**CGGAGCGCC GGG**CTGAAGA TCGCAGCCTT CAACATCCAG 1441 ACATTTGGGG AGACCAAGAT GTCCAATGCC ACCCTCGTCA GCTACATTGT GCAGATCCTG 1501 AGCCGCTACG ACATCGCCCT GGTCCAGGAG GTCAGAGACA GCCACCTGAC TGCCGTGGGG 1561 AAGCTGCTGG ACAACCTCAA TCAGGACGCA CCAGACACCT ATCACTACGT GGTCAGTGAG 1621 CCACTGGGAC GGAACAGCTA TAAGGAGCGC TACCTGTTCG TGTACAGGCC TGACCAGGTG 1681 TCTGCGGTGG ACAGCTACTA CTACGATGAT GGCTGCGAGC CCTGCGGGAA CGACACCTTC 1741 AACCGAGAGC CAGCCATTGT CAGGTTCTTC TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC 1801 ATTGTTCCCC TGCATGCGGC CCCGGGGGAC GCAGTAGCCG AGATCGACGC TCTCTATGAC 1861 GTCTACCTGG ATGTCCAAGA GAAATGGGGC TTGGAGGACG TCATGTTGAT GGGCGACTTC 1921 AATGCGGGCT GCAGCTATGT GAGACCCTCC CAGTGGTCAT CCATCCGCCT GTGGACAAGC 1981 CCCACCTTCC AGTGGCTGAT CCCCGACAGC GCTGACACCA CAGCTACACC CACGCACTGT 2041 GCCTATGACA GGATCGTGGT TGCAGGGATG CTGCTCCGAG GGGCCGTTGT TCCCGACTCG 2101 GCTCTTCCCT TTAACTTCCA GGCTGCCTAT GGCCTGAGTG ACCAACTGGC CCAAGCCATC 2161 AGTGACCACT ATCCAGTGGA GGTGATGCTG AAGTGA

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ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA T Y I C N V N H K P S N T K V D K K 747 729 738 720 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT V E P K S C D K T H T C P P C P A 801 792 783 774 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC 837 846 855 828 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC 900 909 891 882 873 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---954 963 936 945 927 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC 999 1008 1017 990 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG --- --- --- --- --- --- --- --- --- --- ---V L T V L H Q D W L N G K E Y K C K 1071 1080 1035 1044 1053 1062 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA V S N K A L P A P I E K T I S K A K 1098 1107 1116 1125 1089 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG 1170 1179 1161 1143 1152 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC T K N Q V S L T C L V K G 1233 1242 1224 1215 1206 1197 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG I A V E W E S N G Q P E N N Y K T T 1260 1269 1278 1287 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG PPVLDSDGSFFLYSKLTV 1305 1314 1323 1332 1341 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG D K S R W Q Q G N V F S C S V M H E

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1359 · 1368 1377 1386 1395 1404 GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA GGG A L H N H Y T Q K S L S L S P G K G 1449 1413 1422 1431 1440 AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---G G L K I A A F N I Q T F G E T K 1467 1476 1485 1494 1503 ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC M S N A T L V S Y I V Q I L S R Y D 1557 1539 1548 1521 1530 ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG --- --- --- --- --- --- --- --- ---I A L V Q E V R D S H L T A V G K L 1602 1611 1593 1584 CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG 1638 1647 1656 1665 1629 CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC 1701 1710 1719 1728 1692 1683 CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---Q V S A V D S Y Y Y D D G C E P C G 1746 1755 1764 1773 AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---N D T F N R E P A I V R F F S R F T 1791 1800 1809 1818 1827 1836 GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA E V R E F A I V P L H A A P G D A V 1863 1872 1881 1845 1854 GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC A E I D A L Y D V Y L D V Q E K W G 1917 1935 1908 1926 1899 TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA N A G C S Y V R L E D V M L M G D F 1971 1980 1989 1998 1962 1953 CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG --- --- --- --- --- --- --- --- --- --- --- --- --- ---PSQWSSIRLWTSPTFQWL 2007 2016 2025 2034 ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ___ ___ I P D S A D T T A T P T H C A Y D R

2061 2070 2079 2088 2097 2106

ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT

I V V A G M L L R G A V V P D S A L

2115 2124 2133 2142 2151 2160

CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC

P F N F Q A A Y G L S D Q L A Q A I

2169 2178 2187 2196

AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'

S D H Y P V E V M L K *

(A) <u>pAS35</u>

2193 bp 2193 bp DNA PAS35.DNA DEFINITION HUMANISED HMFG1 heavy chain fused to human DNAse construct 35 DEFINITION Clone 17.12.1 with silent K to K mutation (1398 A > G) REFERENCE VERHOEYEN ET AL **AUTHORS** CONSTRUCTION OF RESHAPED HMFG1 etc TITLE IMMUNOL. (1993):78, 364-370 **JOURNAL** Human DNAse sequence is modified as a result of oligo assembly COMMENT (mhdnase.dna) The fusion was made using overlapping oligos AS81 and AS82 COMMENT AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A) **FEATURES** Residue 963 is G > T leading to silent mutation in all clones **FEATURES** In 17.12.1 residue 1398 is A > G (silent K to K mutation) **FEATURES** SITES 410 t 606 g BASE COUNT 500 a 677 c ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG 1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG 1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 1381 CTCTCCCTGT CTCCGAAgGG GAGCGGCGGG CTGAAGATCG CAGCCTTCAA CATCCAGACA 1441 TTTGGGGAGA CCAAGATGTC CAATGCCACC CTCGTCAGCT ACATTGTGCA GATCCTGAGC 1501 CGCTACGACA TCGCCCTGGT CCAGGAGGTC AGAGACAGCC ACCTGACTGC CGTGGGGAAG 1561 CTGCTGGACA ACCTCAATCA GGACGCACCA GACACCTATC ACTACGTGGT CAGTGAGCCA 1621 CTGGGACGGA ACAGCTATAA GGAGCGCTAC CTGTTCGTGT ACAGGCCTGA CCAGGTGTCT 1681 GCGGTGGACA GCTACTACTA CGATGATGGC TGCGAGCCCT GCGGGAACGA CACCTTCAAC 1741 CGAGAGCCAG CCATTGTCAG GTTCTTCTCC CGGTTCACAG AGGTCAGGGA GTTTGCCATT 1801 GTTCCCCTGC ATGCGGCCCC GGGGGACGCA GTAGCCGAGA TCGACGCTCT CTATGACGTC 1861 TACCTGGATG TCCAAGAGAA ATGGGGCTTG GAGGACGTCA TGTTGATGGG CGACTTCAAT 1921 GCGGGCTGCA GCTATGTGAG ACCCTCCCAG TGGTCATCCA TCCGCCTGTG GACAAGCCCC 1981 ACCTTCCAGT GGCTGATCCC CGACAGCGCT GACACCACAG CTACACCCAC GCACTGTGCC 2041 TATGACAGGA TCGTGGTTGC AGGGATGCTG CTCCGAGGGG CCGTTGTTCC CGACTCGGCT 2101 CTTCCCTTTA ACTTCCAGGC TGCCTATGGC CTGAGTGACC AACTGGCCCA AGCCATCAGT 2161 GACCACTATC CAGTGGAGGT GATGCTGAAG TGA

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File: PAS35.DNA
Range: 1 - 2193 Mode: Normal
Codon Table: Universal

FIGURE 8(8)

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ATG (GGA	9 TGG	AGC	TGT	18 ATC	ATC	CTC	27 TTC	TTG	GTA	36 GCA	ACA	GCT	45 ACA	GGT	GTC	54 CAC
M	G	W	s		I	I	L		L	v	A	Т	A	Ţ	G	v	Н
TCC	CAG	63 GTG	CAG	CTG	72 GTG	CAG	тст	81 GGG	GCA	GAG	90 GTG	AAA	AAG	99 CCT	GGG	GCC	108 TCA
s	Q	v	Q	L	v	Q	s	G	Α	E	v	К	K	P	G	Α	S
GTG	AAG	117 GTG	TCC	TGC	126 AAG	GCT	TCT	135 GGC	TAC	ACC	144 TTC	AGT	GCC	153 TAC	TGG	ATA	162 GAG
v		v	s	C	- К	Α	s	G	 Y	T	 F	S	Α	Y	W	I	E
TGG	GTG	171 CGC	CAG	GCT	180 CCA	GGA	AAG	189 GGC	CTC	GAG	198 TGG	GTC	GGA	207 GAG	ATT	TTA	216 CCT
W	v	R	Q	A	P	G	K	G	L	Е	W	v	G	E	I	L	P
GGA	AGT	225 AAT	AAT	TCT	234 AGA	TAC	TAA	243 GAG	AAG	TTC	252 AAG	GGC	CGA	261 GTG	ACA	GTC	270 ACT
G	s	N	N	s	R	Y	N	E	K	F	K	G	R	v	T	v	T
AGA	GAC	279 ACA		ACA	288 AAC		GCC	297 TAC	ATG	GAG	306 CTC		AGC	315 CTG	AGG	TCT	324 GAG
R	D	T	s	T	N	Т	A	Y	М	E	L	s	s	L	R	s	E
GAC	ACA	333 . GCC		TAT	342 TAC		GCA	351 AGA	TCC	TAC	360 GAC		GCC	369 TGG	TTT	GCT	378 TAC
D	Т	Α	V	Y	Y	С	Α	R	S	Y	D	F	A	W	F	Α	Y
TGG	GGC	387 CAA		ACT	396		ACA	405 GTC		TCA	414 GCC		ACC	423 : AAG		CCA	432 TCG
W	G	Q	G	Т	L	V	T	V	S	S	A	S	Т	K	G	P	S
GTC	TTC	441 CCC		GC#	450 450	TCC		459 AAG	AGC	C ACC	468 TCT		GGC	477 ACA		GCC	486 CTG
V	F	P	L	Α	P	s	S	K	S	Т	s	G	G	T	A	Α	L
GGC		495 C CTC	GT(ccc	GA/		GTG	ACC		531 G TCG	TGG	AAC	540 TCA
G	С	L	V	K	D	Y	F	P	Ε	P	V	Т	V	S	W	N	S
GGC		549 C CTC			558 2 GG(GTO		: ACC	TTC		G GC1	GT(585 A CAC	TCC		
G		L												Q			
		60: C TC:	C CT		613 C AG	C GTO			GT			AG		639 C TTC	G GG		
														L			Q

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA T Y I C N V N H K P S N T K V D K K 738 747 720 729 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---765 774 783 792 801 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---E L L G G P S V F L F P P K P K D T 828 837 846 855 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC --- --- --- --- --- --- --- --- --- --- --- --- ---M I S R T P E V T C V V D V S H 900 909 891 873 882 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT EDPEVKFNWYVDGVEVHN 945 954 963 927 936 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC A K T K P R E E Q Y N S T Y R 999 1008 1017 981 990 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG 1062 1071 1080 1053 1044 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA V S N K A L P A P I E K T I S K A K 1098 1107 1116 1125 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG --- --- --- --- --- --- --- --- --- --- --- --- --- ---G Q P R E P Q V Y T L P P S R D E L 1143 1152 1161 1170 1179 1188 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC T K N Q V S L T C L V K G F Y P 1206 1215 1224 1233 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG I A V E W E S N G Q P E N N Y K 1287 1251 1260 1269 1278 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG PPVLDSDGSFFLYSKLTV 1314 1323 1332 1341 1350 1305 GAC AAG AGC AGG TGG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG ___

D K S R W O O G N V F S C S V M H E

1359 1368 1377 1386 1395 1404 GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG AAG GGG AGC --- --- --- --- --- --- --- --- --- --- --- --- --- ---A L H N H Y T Q K S L S P K G S 1413 1422 1431 1440 1449 GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---G G L K I A A F N I Q T F G E T K M 1467 1476 1485 1494 TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC S N A T L V S Y I V Q I L S R Y D I 1566 1557 1548 1521 1530 1539 GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG A L V Q E V R D S H L T A V G K L L 1602 1611 1584 1593 GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA 1647 1656 1665 1638 1629 CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG 1701 1710 1719 1728 1692 1683 GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC V S A V D S Y Y Y D D G C E P C G N 1746 1755 1764 1773 GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA GAG --- --- --- --- --- --- --- --- --- --- --- --- --- ---D T F N R E P A I V R F F S R F T E 1791 1800 1809 1818 1827 1836 GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC V R E F A I V P L H A A P G D A V A 1863 1872 1881 1854 GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG E I D A L Y D V Y L D V Q E K W G L 1908 1926 1935 1899 1917 GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC D F N A G C S Y V R P E D V M L M G 1962 1971 1980 1989 1998 1953 TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC S Q U S S 1 R L W T S P T F Q W L I 2007 2016 2025 2034 2043 2052 CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC ___ ___ __ __ ___ ___ PDSADTTATPTHCAYDRI

2061 2070 2079 2088 2097 2106

GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC

V V A G M L L R G A GC AGC CAC CAA CTG GCC CAA GCC ATC GCC

TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT

F N F Q A A Y G L S D Q L A Q A I S

GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'

D H Y P V E V M L K *

figure 9

(a) pAS36

2190 bp 2190 bp DNA LOCUS HUMANISED HMFG1 heavy chain fused to human DNAse - construct 36 DEFINITION Clone 18.24.1 with residue 1392 T > C DEFINITION REFERENCE AUTHORS VERHOEYEN ET AL CONSTRUCTION OF RESHAPED HMFG1 etc TITLE IMMUNOL. (1993):78, 364-370 **JOURNAL** Human DNAse sequence is modified as a result of oligo assembly COMMENT (mhdnase.dna) The fusion was made using overlapping oligos AS83 and AS84 COMMENT AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A) **FEATURES** Residue 963 is G > T leading to silent mutation in all clones **FEATURES** Residue 1392 T > C silent S to S mutation **FEATURES**

SITES Note
BASE COUNT 498 a 678 c 605 g 409 t
ORIGIN ?

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG 1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG 1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 1381 CTCTCCCTGT CcCCGGGGAG CGGCGGCTG AAGATCGCAG CCTTCAACAT CCAGACATTT 1441 GGGGAGACCA AGATGTCCAA TGCCACCCTC GTCAGCTACA TTGTGCAGAT CCTGAGCCGC 1501 TACGACATCG CCCTGGTCCA GGAGGTCAGA GACAGCCACC TGACTGCCGT GGGGAAGCTG 1561 CTGGACAACC TCAATCAGGA CGCACCAGAC ACCTATCACT ACGTGGTCAG TGAGCCACTG 1621 GGACGGAACA GCTATAAGGA GCGCTACCTG TTCGTGTACA GGCCTGACCA GGTGTCTGCG 1681 GTGGACAGCT ACTACTACGA TGATGGCTGC GAGCCCTGCG GGAACGACAC CTTCAACCGA 1741 GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG TTCACAGAGG TCAGGGAGTT TGCCATTGTT 1801 CCCCTGCATG CGGCCCCGGG GGACGCAGTA GCCGAGATCG ACGCTCTCTA TGACGTCTAC 1861 CTGGATGTCC AAGAGAAATG GGGCTTGGAG GACGTCATGT TGATGGGCGA CTTCAATGCG 1921 GGCTGCAGCT ATGTGAGACC CTCCCAGTGG TCATCCATCC GCCTGTGGAC AAGCCCCACC 1981 TTCCAGTGGC TGATCCCCGA CAGCGCTGAC ACCACAGCTA CACCCACGCA CTGTGCCTAT 2041 GACAGGATCG TGGTTGCAGG GATGCTGCTC CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT 2101 CCCTTTAACT TCCAGGCTGC CTATGGCCTG AGTGACCAAC TGGCCCAAGC CATCAGTGAC 2161 CACTATCCAG TGGAGGTGAT GCTGAAGTGA

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File : PAS36.DNA FIGURE 9 (B) _ 2190 Mode: Normal Codon Table : Universal 45 36 27 18 ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC M G W S C I I L F L V A T A T G 99 108 90 81 TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA <u>S</u> Q V Q L V Q S G A E V K K P G A S 153 144 126 135 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG --- --- --- --- --- --- --- --- --- --- --- --- --- ---189 198 207 180 171 TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT --- --- --- --- --- --- --- --- --- --- --- --- --- ---W V R Q A P G K G L E W V G E I L P 243 252 234 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---315 279 288 297 306 AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG 369 351 360 342 GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC T A V Y Y C A R S Y D 405 414 423 396 TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG 468 459 450 441 GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG 513 531 522 504 GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA G C L V K D Y F P E P V T V S 549 558 567 576 585 GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA 630 621 639 612 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG Y S L S S V V T V P S S S L G T Q 684 693 702 675 666

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA 747 738 720 729 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT --- --- --- --- --- --- --- --- --- --- --- --- ---V E P K S C D K T H T C P P C P A P 792 774 783 765 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---E L L G G P S V F L F P P K P K D T 846 855 837 828 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC $\begin{smallmatrix} L & M & I & S & R & T & P & E & V & T & C & V & V & D & V & S & H \\ \end{smallmatrix}$ 900 882 891 873 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---E D P E V K F N W Y V D G V E 963 945 954 936 927 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---K T K P R E E Q Y N S T Y R V V S 1008 990 999 981 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG --- --- --- --- --- --- --- --- --- --- --- --- --- ---V L T V L H Q D W L N G K E Y K C K 1035 1044 1053 1062 1071 1080 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA --- --- --- --- --- --- --- --- --- --- --- --- ---V S N K A L P A P I E K T I S K A K 1089 1098 1107 1116 1125 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG --- --- --- --- --- --- --- --- --- --- --- --- ---1179 1143 1152 1161 1170 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC T K N Q V S L T C L V K G F Y P S D 1233 1215 1224 1206 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG P E N N Y K T T I A V E W E S N G Q 1278 1269 1260 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG --- --- --- --- --- --- --- --- --- --- --- --- --- ---PPVLDSDGSFFLYSKLTV 1305 1314 1323 1332 1341 1350 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG --- --- --- --- --- --- --- --- --- --- ---D K S R W Q Q G N V F S C S V M H E

1368 1377 1386 1395 1404 1359 GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCC CCG GGG AGC GGC A L H N H Y T Q K S L S P G S G 1449 1440 1422 1431 1413 GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG TCC --- --- --- --- --- --- --- --- --- --- --- --- ---1494 1503 1467 1476 1485 AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC GCC N A T L V S Y I V Q I L S R Y D I A 1557 1530 1539 1548 CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG GAC L V Q E V R D S H L T A V G K L L D 1611 1602 1584 1593 AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA CTG 1647 1656 1665 1638 1629 GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG GTG 1719 1701 1710 1692 1683 TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC GAC 1746 1755 1764 1773 1782 1737 ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA GAG GTC T F N R E P A I V R F F S R F T E V 1800 1809 1818 1827 1836 1791 AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC GAG E F A I V P L H A A P G D A V A E 1863 1872 1881 1845 1854 ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG GAG I D A L Y D V Y L D V Q E K W G L E 1935 1926 1908 1917 GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC TCC G C S D V M L M G D F N A 1989 1980 1962 1971 CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC CCC --- --- --- --- --- --- --- --- --- --- --- --- ---Q W S S I R L W T S P T F Q W L I P 2007 2016 2025 2034 2043 2052 GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC GTG

2061 2070 2079 2088 2097 2106
GTT GCA GGG ATG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC TTT

V A G M L L R G A V V P D S A L P F

2115 2124 2133 2142 2151 2160
AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT GAC

N F Q A A Y G L S D Q L A Q A I S D

2169 2178 2187
CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'
H Y P V E V M L K *

FIGURE 10

(A) pAS37

2196 bp 2196 bp DNA PAS37.DNA 2226 bp DEFINITION HUMANISED HMFG1 heavy chain fused to human DNAse construct 37 DEFINITION Clone 16.4.2 (same as hcdnasel.dna template file) plus NLS REFERENCE VERHOEYEN ET AL **AUTHORS** CONSTRUCTION OF RESHAPED HMFG1 etc TITLE IMMUNOL. (1993):78, 364-370 JOURNAL Human DNAse sequence is modified as a result of oligo assembly COMMENT (mhdnase.dna) The fusion was made using overlapping oligos AS79 and AS80 COMMENT AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A) **FEATURES** Residue 963 is G > T leading to silent mutation in all clones **FEATURES** SITES Note 619 q 413 t BASE COUNT 511 a 683 c ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 781 TTCCTCTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG 1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG 1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 1381 CTCTCCCTGT CTCCGGGTAA AGGGAGCGGC GGGCTGAAGA TCGCAGCCTT CAACATCCAG 1441 ACATTTGGGG AGACCAAGAT GTCCAATGCC ACCCTCGTCA GCTACATTGT GCAGATCCTG 1501 AGCCGCTACG ACATCGCCCT GGTCCAGGAG GTCAGAGACA GCCACCTGAC TGCCGTGGGG 1561 AAGCTGCTGG ACAACCTCAA TCAGGACGCA CCAGACACCT ATCACTACGT GGTCAGTGAG 1621 CCACTGGGAC GGAACAGCTA TAAGGAGCGC TACCTGTTCG TGTACAGGCC TGACCAGGTG 1681 TCTGCGGTGG ACAGCTACTA CTACGATGAT GGCTGCGAGC CCTGCGGGAA CGACACCTTC 1741 AACCGAGAGC CAGCCATTGT CAGGTTCTTC TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC 1801 ATTGTTCCCC TGCATGCGGC CCCGGGGGAC GCAGTAGCCG AGATCGACGC TCTCTATGAC 1861 GTCTACCTGG ATGTCCAAGA GAAATGGGGC TTGGAGGACG TCATGTTGAT GGGCGACTTC 1921 AATGCGGGCT GCAGCTATGT GAGACCCTCC CAGTGGTCAT CCATCCGCCT GTGGACAAGC 1981 CCCACCTTCC AGTGGCTGAT CCCCGACAGC GCTGACACCA CAGCTACACC CACGCACTGT 2041 GCCTATGACA GGATCGTGGT TGCAGGGATG CTGCTCCGAG GGGCCGTTGT TCCCGACTCG 2101 GCTCTTCCCT TTAACTTCCA GGCTGCCTAT GGCCTGAGTG ACCAACTGGC CCAAGCCATC 2161 AGTGACCACT ATCCAGTGGA GGTGATGCTG AAGGGGGGCG GACCCAAAAA GAAGCGCAAG 2221 **GTTTGA**

LONLS

File: PAS37.DNA
Range: 1 - 2226 Mode: Normal
Codon Table: Universal

5

FIGURE 10 (B)

														- 0 .c.		, (0	,
ATG	GGA	9 TGG	AGC	TGT	18 ATC	ATC	CTC	27 TTC '	TTG	GTA	36 GCA	ACA			GGT		54
 M	 G		s					 F	 L	 V	 A	т	Α	T	G	V	Н
TCC	CAG	63 GTG	CAG	CTG	72 GTG	CAG	тст	81 GGG	GCA	GAG	90 GTG	AAA	AAG	99 CCT	GGG	GCC	108 TC#
 S	Q	v	Q	 L	v	Q	s	G	Α	E	v	 К	K	P	G	Α	s
GTG	AAG	117 GTG	TCC	TGC	126 AAG		TCT	135 GGC		ACC	144 TTC	AGT	GCC	153 TAC	TGG	ATA	162 GAG
 V	 К	v	s	 С	 К	 A	 S	 G	 У	 Т	 F	s	Α	Y	w	1	E
TGG	GTG	171 CGC	CAG	GCT	180 CCA	GGA	AAG		CTC	GAG	198 TGG	GTC	GGA	207 GAG	АТТ	TTA	21 CC
w	v	R	Q	Α	P	G	K	G		E	W	v	G	E	I	L	P
GGA	AGT	225 AAT	AAT	TCT	234 AGA	TAC	ААТ	243 GAG	AAG	TTC	252 AAG	GGC	CGA	261 GTG	ACA	GTC	27 AC
G	s	N	N	s	R	Y	N	E	к	F	K	G	R	v	T	v	T
AGA	GAC	279 ACA		: ACA	288 . AAC		GCC			GAG	306 CTC		AGC	315 CTG		TCT	32 GA
R	D	T	s	Т	N	T	Α	Υ		E	L	s	s	L	R	s	E
GAC	AC#	333 4 GCC		TAT C	342 TAC		GCA	351 AGA	TCC	TAC	360 GAC		GCC	369 TGG		GCT	37 TA
D	Т	A	v	Y	Y	С	A	R	s	Y	D	F	А	W	F	A	Y
TGG	GGG	387 C CA		G ACT	396 CTC		: ACA	405 GTC	TCC	TCA	414 4 GCC		C ACC	423 AAG		CCA	43 TO
W	G	Q	G	T	L	V	\mathbf{T}	V	S	s	A	S	T	K	G	P	5
GTC	TTC	44: C CC		G GC	450 A CCC		TCC	459 : AAG		C ACC	468 TC1		GGC	477 C ACA		GCC	48 C C 1
V	F	P	L	Α	P	s	s	K	s	T	s	G	G	Т	Α	Α	Ι
GGG		49 C CT	G GT	C AA	504 G GAG	C TAC	C TTC		GA/	A CC	522 G GTC		G GTC	53: G TC(AA(54 C TC
G										P	V	Т	V	s	W	N	:
GG	C GC	54 C CT		C AG	55: C GG	C GT	G CAG		TTC	c cc	576 G GC'		C CT/	58: A CA		C TC	5 9 A G
G	A	L	T	S	 G					P	A	V	L	Q	s	S	(
CT	C TA	60 C TC		C AG	61 C AG		G GT	621 G ACC		G CC			C AG	63 C TT		C AC	6 C C
L	 Y	' S	L	, s	s	V	V	т	V	P	S	s	S	L	G	Т	

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAA T Y I C N V N H K P S N T K V D K K 729 747 720 738 711 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT V E P K S C D K T H T C P P C P A P 774 783 792 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC E L L G G P S V F L F P P K P K D T 855 819 828 837 846 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC M I S R T P E V T C V V D V S H 882 891 900 909 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT E D P E V K F N W Y V D G V E V H N 927 936 945 954 963 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC --- --- --- --- --- --- --- --- --- --- --- --- ---A K T K P R E E Q Y N S T Y R V V S 999 990 1008 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG V L T V L H Q D W L N G K E Y K C K 1044 1053 1062 1071 1080 1035 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA V S N K A L P A P I E K T I S K A K 1098 1107 1116 1089 1125 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG 1152 1161 1170 1179 1143 1188 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC T K N Q V S L T C L V K G F Y 1206 1215 1224 1233 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG --- --- --- --- --- --- --- --- --- --- ---I A V E W E S N G Q P E N N Y K T T 1260 1269 1278 1287 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG P P V L D S D G S F F L Y S K L T V 1314 1323 1332 1341 1350 1305 GAC AAG AGC AGG TGG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG --- --- --- --- --- --- --- --- ---D K S R W Q Q G N V P S C S V M H E

1377 1386 1395 1404 1359 1368 GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA GGG A L H N H Y T Q K S L S L S P G K G 1422 1449 1431 1440 1413 AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---S G G L K I A A F N I Q T F G E T K 1494 1503 1485 1476 1467 ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---M S N A T L V S Y I V Q I L S R Y D 1548 1557 1539 1530 ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG --- --- --- --- --- --- --- --- --- --- --- --- ---I A L V Q E V R D S H L T A V G K L 1575 1584 1593 1602 1611 1620 CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---1638 1647 1656 1665 1629 CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---P L G R N S Y K E R Y L F V Y R P D 1683 1692 1701 1710 1719 CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG --- --- --- --- --- --- $\begin{smallmatrix} Q & V & S & A & V & D & S & Y & Y & P & D & G & C & E & P & C & G \\ \end{smallmatrix}$ 1773 1764 1746 1755 1737 AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA N D T F N R E P A I V R F F S R F T 1818 1827 1800 1809 1791 GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA 1863 1872 1881 1890 1854 1845 GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC A E I D A L Y D V Y L D V Q E K W G 1899 1908 1917 1926 1935 TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA --- --- --- --- --- --- --- --- --- --- --- --- --- ---L E D V M L M G D F N A G C S Y V R 1980 1989 1962 1971 1953 CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG PSQWSSIRLWTSPTFQWL 2025 2034 2043 2016 ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG I P D S A D T T A T P T H C A Y D R

2061 2070 2079 2088 2097 2106

ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT

I V V A G M L L R G A V V P D S A L

2115 2124 2133 2142 2151 2160

CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC

P F N F Q A A Y G L S D Q L A Q A I

2169 2178 2187 2196 2205 2214

AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG

S D H Y P V E V M L K G G G P K K K

2223 CGC AAG GTT TGA 3'

(A) pAS38

14-AUG-1998 DNA 2223 bp 2193 bp PAS38.DNA DEFINITION HUMANISED HMFG1 heavy chain fused to human DNAse construct 38 DEFINITION Clone 17.12.1 with silent K to K mutation (1398 A > G)+NLS REFERENCE VERHOEYEN ET AL **AUTHORS** CONSTRUCTION OF RESHAPED HMFG1 etc TITLE IMMUNOL. (1993):78, 364-370 JOURNAL Human DNAse sequence is modified as a result of oligo assembly COMMENT (mhdnase.dna) The fusion was made using overlapping oligos AS81 and AS82 COMMENT AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A) **FEATURES** Residue 963 is G > T leading to silent mutation in all clones **FEATURES** In 17.12.1 residue 1398 is A > G (silent K to K mutation) **FEATURES** SITES Note 683 c 618 g 412 t 510 a BASE COUNT ORIGIN ?

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG 1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG 1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 1381 CTCTCCCTGT CTCCGAAg<mark>GG GAGCGGCGGG</mark> CTGAAGATCG CAGCCTTCAA CATCCAGACA 1441 TTTGGGGAGA CCAAGATGTC CAATGCCACC CTCGTCAGCT ACATTGTGCA GATCCTGAGC 1501 CGCTACGACA TCGCCCTGGT CCAGGAGGTC AGAGACAGCC ACCTGACTGC CGTGGGGAAG 1561 CTGCTGGACA ACCTCAATCA GGACGCACCA GACACCTATC ACTACGTGGT CAGTGAGCCA 1621 CTGGGACGGA ACAGCTATAA GGAGCGCTAC CTGTTCGTGT ACAGGCCTGA CCAGGTGTCT 1681 GCGGTGGACA GCTACTACTA CGATGATGGC TGCGAGCCCT GCGGGAACGA CACCTTCAAC 1741 CGAGAGCCAG CCATTGTCAG GTTCTTCTCC CGGTTCACAG AGGTCAGGGA GTTTGCCATT 1801 GTTCCCCTGC ATGCGGCCCC GGGGGACGCA GTAGCCGAGA TCGACGCTCT CTATGACGTC 1861 TACCTGGATG TCCAAGAGAA ATGGGGCTTG GAGGACGTCA TGTTGATGGG CGACTTCAAT 1921 GCGGGCTGCA GCTATGTGAG ACCCTCCCAG TGGTCATCCA TCCGCCTGTG GACAAGCCCC 1981 ACCTTCCAGT GGCTGATCCC CGACAGCGCT GACACCACAG CTACACCCAC GCACTGTGCC 2041 TATGACAGGA TCGTGGTTGC AGGGATGCTG CTCCGAGGGG CCGTTGTTCC CGACTCGGCT 2101 CTTCCCTTTA ACTTCCAGGC TGCCTATGGC CTGAGTGACC AACTGGCCCA AGCCATCAGT 2161 GACCACTATC CAGTGGAGGT GATGCTGAAG GGGGGCGGAC CCAAAAAGAA GCGCAAGGTT 2221 <u>TGA</u>

LOMES

File : PAS38.DNA 2223 Mode : Normal FICURE 11 (B) Codon Table : Universal 36 45 18 27 ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC --- --- --- --- --- --- --- --- --- --- --- --- ---G W S C I I L F L V A T A T G V H 72 81 99 90 TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA S Q V Q L V Q S G A E V K K P G A S 126 135 144 117 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG --- --- --- --- --- --- --- --- --- --- --- --- --- ---V K V S C K A S G Y T F S A Y W I E 207 189 198 171 180 TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT --- --- --- --- --- --- --- --- --- --- --- --- --- ---W V R Q A P G K G L E W V G E I L P 261 243 252 234 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT G S N N S R Y N E K F K G R V T V T 306 315 288 297 AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG --- --- --- --- --- --- --- --- --- --- --- --- ---R D T S T N T A Y M E L S 351 360 369 342 333 GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC 405 414 423 396 TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- $\hbox{\tt W} \hbox{\tt G} \hbox{\tt Q} \hbox{\tt G} \hbox{\tt T} \hbox{\tt L} \hbox{\tt V} \hbox{\tt T} \hbox{\tt V} \hbox{\tt S} \hbox{\tt S} \hbox{\tt A} \hbox{\tt S} \hbox{\tt T} \hbox{\tt K} \hbox{\tt G} \hbox{\tt P} \hbox{\tt S}$ 441 450 459 468 GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG V F P L A P S S K S T S G G T A A L 513 522 495 504 GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA 567 576 585 558 GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA 621 630 639 612 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG ______ L Y S L S S V V T V P S S S L G T Q 693 702 666 675 684 657

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA T Y I C N V N H K P S N T K V D K K 711 720 729 738 747 756 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT EPKSCDKTHTCP 765 774 783 792 801 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC --- --- --- --- --- --- --- --- --- --- --- --- --- ---E L L G G P S V F L F P P K P K D T 828 837 846 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---LMISRTPEVTCVVDVSH 882 891 900 909 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---927 936 945 954 963 972 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---A K T K P R E E Q Y N S T Y R V V S 981 990 999 1008 1017 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG V L T V L H Q D W L N G K E Y K C K 1035 1044 1053 1062 1071 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA --- --- --- --- --- --- --- --- --- --- --- --- ---V S N K A L P A P I E K T I S K A K 1089 1098 1107 1116 1125 1134 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG G Q P R E P Q V Y T L P P S R D E L 1152 1161 1170 1179 1188 1143 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC T K N Q V S L T C L V K G F Y P S D 1197 1206 1215 1224 1233 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG --- --- --- --- --- --- --- --- --- --- --- ---I A V E W E S N G Q P E N N Y K 1251 1260 1269 1278 1287 1296 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---PVLDSDGSFFLYSKLTV 1305 1314 1323 1332 1341 1350 GAC AAG AGC AGG TGG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG D K S R W Q Q G N V F S C S V M H E

1386 1395 1377 1359 1368 . GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG AAG GGG AGC A L H N H Y T Q K S L S P K G S 1422 1431 1440 1413 GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG G G L K I A A F N I Q T F G E T K M 1467 1476 1485 1494 1503 1512 TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC S N A T L V S Y I V Q I L S R Y D I 1548 1530 1539 1557 1521 GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG A L V Q E V R D S H L T A V G K L L 1593 1602 1611 1575 1584 GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA D N L N Q D A P D T Y H Y V V S E P 1638 1647 1656 1665 1629 CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG L G R N S Y K E R Y L F V Y R P D Q 1692 1701 1710 1719 GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC 1746 1755 1764 1773 1737 GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG T F N R E P A I V R F F S R F T E 1809 1818 1827 1800 GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC V R E F A I V P L H A A P G D A V A 1845 1854 1863 1872 1881 1890 GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG --- --- --- --- --- --- $\hbox{\tt E} \quad \hbox{\tt I} \quad \hbox{\tt D} \quad \hbox{\tt A} \quad \hbox{\tt L} \quad \hbox{\tt Y} \quad \hbox{\tt D} \quad \hbox{\tt V} \quad \hbox{\tt Y} \quad \hbox{\tt L} \quad \hbox{\tt D} \quad \hbox{\tt V} \quad \hbox{\tt Q} \quad \hbox{\tt E} \quad \hbox{\tt K} \quad \hbox{\tt W} \quad \hbox{\tt G} \quad \hbox{\tt L}$ 1908 1917 1926 1935 GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC E D V M L M G D F N A G C S Y V R P 1971 1980 1989 1953 1962 TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC 2034 2025 2043 2016 CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC ___ __ __ __ __ __ __ __ __ __ __ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ P D S A D T T A T P T H C A Y D R I

2061 2070 2079 2088 2097 2106

GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC

V V A G M L L R G A V V P D S A L P

2115 2124 2133 2142 2151 2160

TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT

F N F Q A A Y G L S D Q L A Q A I S

2169 2178 2187 2196 2205 2214

GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG CGC

D H Y P V E V M L K G G G G G P K K K K R

2223
AAG GTT TGA 3'
--- --- K V *

FIGURE 12

(A) pAS39

14-AUG-1998 2220 bp 2190 bp DNA PAS39.DNA HUMANISED HMFG1 heavy chain fused to human DNAse - construct 39 DEFINITION DEFINITION Clone 18.24.1 with residue 1392 T > C +NLS REFERENCE VERHOEYEN ET AL **AUTHORS** CONSTRUCTION OF RESHAPED HMFG1 etc TITLE IMMUNOL. (1993):78, 364-370 JOURNAL Human DNAse sequence is modified as a result of oligo assembly COMMENT (mhdnase.dna) The fusion was made using overlapping oligos AS83 and AS84 COMMENT AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A) **FEATURES** Residue 963 is G > T leading to silent mutation in all clones **FEATURES** Residue 1392 T > C silent S to S mutation **FEATURES** SITES Note 684 c 617 g 411 t 508 a BASE COUNT ? ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG 1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG 1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 1381 CTCTCCCTGT CcCCGGGGAG CGGCGGGCTG AAGATCGCAG CCTTCAACAT CCAGACATTT 1441 GGGGAGACCA AGATGTCCAA TGCCACCCTC GTCAGCTACA TTGTGCAGAT CCTGAGCCGC 1501 TACGACATCG CCCTGGTCCA GGAGGTCAGA GACAGCCACC TGACTGCCGT GGGGAAGCTG 1561 CTGGACAACC TCAATCAGGA CGCACCAGAC ACCTATCACT ACGTGGTCAG TGAGCCACTG 1621 GGACGGAACA GCTATAAGGA GCGCTACCTG TTCGTGTACA GGCCTGACCA GGTGTCTGCG 1681 GTGGACAGCT ACTACTACGA TGATGGCTGC GAGCCCTGCG GGAACGACAC CTTCAACCGA 1741 GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG TTCACAGAGG TCAGGGAGTT TGCCATTGTT 1801 CCCCTGCATG CGGCCCCGGG GGACGCAGTA GCCGAGATCG ACGCTCTCTA TGACGTCTAC 1861 CTGGATGTCC AAGAGAAATG GGGCTTGGAG GACGTCATGT TGATGGGCGA CTTCAATGCG 1921 GGCTGCAGCT ATGTGAGACC CTCCCAGTGG TCATCCATCC GCCTGTGGAC AAGCCCCACC 1981 TTCCAGTGGC TGATCCCCGA CAGCGCTGAC ACCACAGCTA CACCCACGCA CTGTGCCTAT 2041 GACAGGATCG TGGTTGCAGG GATGCTGCTC CGAGGGGCCCG TTGTTCCCGA CTCGGCTCTT 2101 CCCTTTAACT TCCAGGCTGC CTATGGCCTG AGTGACCAAC TGGCCCAAGC CATCAGTGAC 2161 CACTATCCAG TGGAGGTGAT GCTGAAGGGG GGCGGACCCA AAAAGAAGCG CAAGGTTTGA

File: PAS39.DNA
Range: 1 - 2220 Mode: Normal
Codon Table: Universal

FIGURE 12(B)

								27			5	36	•	-	45		· ,	,	54	
ATG	GGA	TGC) G AGO	TG	18 T ATC	ATC	CTC	TTC	TTC	G GT	A G	CA A	ACA	GCT	ACA	. GG	Т G	TC	CAC	
 M	 G	 W	 S				L			 V		A	T	A	Т	G		<u>v_</u>	Н_	
	040	6: GT(3 G. CA(G CT	7 G GT	2 G CAG	G TC	81 r gg(L G GC	A GA		90 TG	AAA	AAG	99 CC1		G (GCC	108 TCA	
	 Q							 G				 V	 K	 К	P			Α	S	
			7 'G TC	C TO	12 GC AA	6 .g gc	т тс	13 T GG	5 C TA	C AC	1 CC T	44 CTC	AGT	GCC	15: TA		GG .	АТА	162 GAG	
 V	 K										 T	F	 S	- - -	Y		w W	I	E	
				AG G	18 CT C	30 CA GO	SA AA	18 4G GG	19 FC C 1	rc g	AG '	198 IGG	GTC	: GG	20 A GA		тт	TTA	21 CC	
 W	 V						 3 F				· E	 W		G	 E		I	L	P	
				-		2.4		24 AT G	13 AG A	AG I	TC	252 AAG	GGC	c cg	26 A G7		ACA	GTC	27 AC	
 G		 S								 K	F		G	 R		 J	т	V	 1	
			70			.88 .AC A	.CA G	2 CC T	97 ac <i>a</i>	TG (GAG	306 CTC	S AG	C AG		15 TG /	AGG	TC		24 AG
 R		AC F D	T	·	 T	 N				 М	 E		 S			 L	 R	s		- - E
		_		GTC '	TAT	342 rac 1	GT C	3 SCA <i>P</i>	51 GA '				C TT		CC T	_	TTI F	GC 	T T	78 AC Y
Ι)	Т	Α	V	Y	Y	С	A	R	S	Y	D			-	W 123	ı			32
TY	GG (GGC	387 CAA	GGG	ACT	396 CTG (GTC	ACA (405 GTC	TCC	TCA	41 GC	4 C T(CC A					r A:	CG
_	W	G	Q	G	T	L	V	Т	٧	S	s	A		S	Т	K	G	F		S
G	TC	TTC	441 CCC	CTG	GCA	450 CCC	TCC	TCC	459 AAG	AGC	ACC	46 TO	T G	GG (GC .	477 ACA 	GC 	G G(486 CTG
-	V	F	P	L	A	P	S	S	K	S	Т	:	5	G	G	Т	A		A	L
C	GC	TGC	495 CTG	GTC	AAG	504 GAC	TAC	TTC	513 CCC	GAA	, cc	G G	22 TG A	CG (531 TCG	TO	SG A	AC	540 TCA
	 G	C	 L	V		D	Y	F	P	E	P		V	Т	V	S	V	٧	N	S
	GGC	GCC	549 CTG	1.00	: AGC	558 GGC	GTG.	CAC	ACC	TTC	c cc	G G	CT (GTC	СТА	585 CAC	T T	CC 1	CA	594 GG
	 G				. AGC S															
	CTC	: TAC	603 TC0		C AG0	612 C AGC	· care	: GTG	621 ACC	GT	G C	ac s	530 rcc	AGC	AGC	63°	G G	GC 4	4CC	64 CA
	I.	Y	s	 L	 S	s	V	V	Т	V		P	s	s	S	L		G	Т	Q
			65	7		660	5		67	5			684			69	3			70

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ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA T Y I C N V N H K P S N T K 729 738 720 711 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT ___ ___ V E P K S C D K T H T C P P C P A P 783 792 801 774 765 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC ___ __ __ __ LGGPSVFLFPPKPKDT 837 855 819 828 846 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC MISRTPEVTCVVDVSH 882 891 900 909 873 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT EDPEVKFNWYVDGVEVHN 954 963 927 936 945 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC 999 1008 1017 981 990 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG --- --- --- --- --- --- --- --- --- --- --- --- ---L H Q D W L N G K E Y K C 1053 1062 1071 1035 1044 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA V S N K A L P A P I E K T I S K A K 1134 1089 1098 1107 1116 1125 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG G Q P R E P Q V Y T L P P S R D E L 1152 1161 1170 1179 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ___ __ __ __ __ __ __ __ ___ ___ ___ 1206 1215 1224 1233 1242 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG I A V E W E S N G Q P E N N 1251 1260 1269 1278 1287 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG ___ ___ P V L D S D G S F F L Y S K L T V 1323 1332 1341 1314 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG --- --- --- --- --- --- --- --- --- --- --- --- ---

1359 1368 1377 1386 1395 *GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCC CCG GGG AGC GGC A L H N H Y T Q K S L S P 1422 1431 1440 1449 GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG TCC G L K I A A F N I Q T F G E T K M S 1467 1476 1485 1494 1503 1512 AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC GCC N A T L V S Y I V Q I L S R Y D I A 1548 1530 1539 CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG GAC V Q E V R D S H L T A V G K L L D 1584 1593 1602 1611 AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA CTG N L N Q D A P D T Y H Y V V S E P L 1629 1638 1647 1656 1665 GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG GTG G R N S Y K E R Y L F V Y R P D O V 1701 1683 1692 1710 1719 TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC GAC S A V D S Y Y Y D D G C E P C G N D 1737 1746 1755 1764 1773 1782 ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA GAG GTC F N R E P A I V R F F S R F T E V 1791 1800 1809 1818 1827 1836 AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC GAG E F A I V P L H A A P G D A V A E 1854 1863 1872 1845 1881 1890 ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG GAG --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---I D A L Y D V Y L D V Q E K W G L E 1899 1908 1917 1926 1935 GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC TCC D V M L M G D F N A G C S Y V R P S 1971 1980 1989 1953 1962 CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC CCC --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---Q W S S I R L W T S P T F Q W L I P 2007 2016 2025 2034 2043 GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC GTG D S A D T T A T P T H C A Y D R I V

GTT TGA 3'

<u>v</u> *

FIGURE 13

(A) pAS101

06-MAR-1995 mRNA PRI 1548 bp PAS101.DNA DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS101) ACCESSION NID DNase I. KEYWORDS DNase I sequence is from assembled oligos (thus modified c/f SOURCE MHDNASE1.dna) ORGANISM Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L. **AUTHORS** Recombinant human DNase I reduces the viscosity of cystic fibrosis TITLE Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990) **JOURNAL** 91067672 MEDLINE 308 t 430 g BASE COUNT 343 a 467 c ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAG GCGGGCTGAA GATCGCAGCC 781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT 841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG 901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC 961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG 1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG 1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC 1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC CGAGATCGAC 1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG 1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC 1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA 1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT 1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG 1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGTGA

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. Figure 13 (B)

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SYN
                                                             25-AUG-2000
                       1548 BP SS-DNA
           FDDNASE101
LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
                     Location/Qualifiers
FEATURES
                     join(1..>720,<781..1548)
     frag
                     /note="1 to 1548 of PAS101.dna [Split]"
                     721..780
     frag
                     /note="1 to 60 of 101/105linker"
                     join(721..>735,<736..>759,<760..>780)
     frag
                     /note="1 to 80 of 102linker [Split]"
                                           309 T
                                  431 G
                        465 C
                343 A
BASE COUNT
ORIGIN
        1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
77.
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGTCC ACCGTGTCCA GCACCAGAGG GCGGGCTGAA GATCGCAGCC
      781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT
      841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
      901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
      961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
     1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
     1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC
     1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC CGAGATCGAC
     1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
     1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC
     1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
     1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
     1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
     1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGTGA
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11

Figure 13c

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1557 BP SS-DNA
                                                    SYN
                                                              29-AUG-2000
LOCUS
            FDDNASE101
DEFINITION
ACCESSION
KEYWORDS
SOURCE
                     Location/Qualifiers
FEATURES
                     10.,1557
     frag
                     /note="1 to 1548 of FdDNase101correct"
                     join(10..>729,<790..1557)
     frag
                     /note="1 to 1548 of PAS101.dna [Split]"
                     730..789
     fraq
                     /note="1 to 60 of 101/105linker"
                     join(730..>744,<745..>768,<769..>789)
     frag
                     /note="1 to 80 of 102linker [Split]"
                                           309 T
                         471 C
BASE COUNT
                                  433 G
                344 A
ORIGIN
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG CGGGCTGAAG
      781 ATCGCAGCCT TCAACATCCA GACATTTGGG GAGACCAAGA TGTCCAATGC CACCCTCGTC
      841 AGCTACATTG TGCAGATCCT GAGCCGCTAC GACATCGCCC TGGTCCAGGA GGTCAGAGAC
      901 AGCCACCTGA CTGCCGTGGG GAAGCTGCTG GACAACCTCA ATCAGGACGC ACCAGACACC
      961 TATCACTACG TGGTCAGTGA GCCACTGGGA CGGAACAGCT ATAAGGAGCG CTACCTGTTC
     1021 GTGTACAGGC CTGACCAGGT GTCTGCGGTG GACAGCTACT ACTACGATGA TGGCTGCGAG
     1081 CCCTGCGGGA ACGACACCTT CAACCGAGAG CCAGCCATTG TCAGGTTCTT CTCCCGGTTC
     1141 ACAGAGGTCA GGGAGTTTGC CATTGTTCCC CTGCATGCGG CCCCGGGGGA CGCAGTAGCC
     1201 GAGATCGACG CTCTCTATGA CGTCTACCTG GATGTCCAAG AGAAATGGGG CTTGGAGGAC
     1261 GTCATGTTGA TGGGCGACTT CAATGCGGGC TGCAGCTATG TGAGACCCTC CCAGTGGTCA
     1321 TCCATCCGCC TGTGGACAAG CCCCACCTTC CAGTGGCTGA TCCCCGACAG CGCTGACACC
     1381 ACAGCTACAC CCACGCACTG TGCCTATGAC AGGATCGTGG TTGCAGGGAT GCTGCTCCGA
      1441 GGGGCCGTTG TTCCCGACTC GGCTCTTCCC TTTAACTTCC AGGCTGCCTA TGGCCTGAGT
      1501 GACCAACTGG CCCAAGCCAT CAGTGACCAC TATCCAGTGG AGGTGATGCT GAAGTGA
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File: PAS101.DNA
Range: 1 - 1548 Mode: Normal
Codon Table: Universal

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FICURE 13(D)

			9			18			o m	27	DOV.	CT	יא (36		. GC		45 CA (GGT	GTO		4 C
ATG					TGT C					 F				 A		 A		 T	 G			
М	G		W 63	3	C	72				81				90				99			10	08
TCC	CA	G G	TG	CAG	CTG	GTO	CAG		т		GCA	4 G <i>I</i>	AG ∙	GTG 	AA.	A. A.	.G C	CT	GGG 	GC	C T(CA
S	Q		V	Q	L	V	Q	2	5	G	Α	1	Е	V	K	ŀ	<	P	G	A	. :	S
CTC	4 4	G (17	TCC	TGO	12 : AA	6 G GC	T T	: TC (135 GGC		C A		144 TTC		T GO		L53 PAC	TGG	ra :		62 AG
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			171			18	0			189				198	3			207				16
TGG	G:	rg (CGC	CAG	GC'		A GO															
W	1	J	R	Q	A	F	• (3	K	G	L	ı	Е									
GG <i>I</i>	A A	GT	225 AAT	AA	г тс	23 T AC	4 3A T	AC A	TA	243 GAG	AA	√G T	rtc	25: AA	G G	GC C		261 GTG		A G		270 ACT
- - -		 s		N	 S		₹			 E				 K		 G	R	v	Т		v .	T
			279)		2				297	,	n C	0 3 0			cc i		315		ദേസ		324 GAG
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R		D		s		ר י				Y 25.						5			9			378
GA	C I	ACA	GC(3 C GI		T TA	42 AC 1 	GT	GCA	AG.	A T	CC	AT	G <i>G</i>	AC 1	TT	GCC					TAC
 D)	Т	A	<i>\</i>			Y						Y	Ī)	F	Α	W	3	7	A	Y
Tr.C	7C	ccc	38	7 A GO	A DE	3 Ст (96 TG (GTC	ACA	40 4 GT		rcc			14 CC 1		ACC			GC (CCA	432 TCG
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			4.4	. 1			150			45	59				68			47				486
_																						CTG
	V	F]	?	L	A	Р													А	А	L 540
G	GC	TG	4 ! C C'	95 TG 6	STC .	AAG	504 GAC		ТТ	C C	CC ·	GAA	CC	G (322 GTG		GT	G T	31 CG 7	rgg	AAC	TCA
-	G	~ - C		 L		 К		Y												W	N	S
,	200	00	5	49	۸۵۵	NGC	558 GGC	ርጥር	C			тто			576 GCT	GTC	CT		0.5		TC	594 A GGA
	 																					 G

621 630 639 612 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG ___ ___ __ __ __ __ __ __ __ __ __ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ 675 684 693 657 666 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA T Y I C N V N H K P S N T K V D K K 711 720 729 738 747 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT V E P K S C D K T H T C P P C P A P 765 774 783 792 801 GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ___ E G G L K I A A F N I Q T F G E T K 837 846 855 819 828 ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC S N A T L V S Y I V Q I L S R Y D 900 909 882 891 873 ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG I A L V Q E V R D S H L T A V G K L 927 936 945 954 CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG L D N L N Q D A P D T Y H Y V V S E 999 1008 1017 990 CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC R Y L F V Y R N S Y K E 1044 1053 1062 1071 1035 CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG Q V S A V D S Y Y Y D D G C E P C G 1107 1116 1125 1098 AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA D T F N R E P A I V R F F S R F T 1170 1179 1152 1161 1143 GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA E V R E F A I V P L H A A P G D A V 1197 1206 1215 1224 1233 1242

GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC --- --- --- --- --- --- --- --- --- --- --- --- ---A E I D A L Y D V Y L D V Q E K W 1251 1260 1269 1278 1287 1296 TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA --- --- --- --- --- --- --- --- --- --- --- ---L E D V M L M G D F N A G C S Y V R 1305 1314 1323 1332 1341 1350 CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG --- --- --- --- --- --- --- --- --- --- ---PSQWSSIRLWTSPTFQWL 1359 1368 1377 1386 1395 1404 ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG I P D S A D T T A T P T H C A Y D R 1413 1422 1431 1440 1449 1458 ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT --- --- --- --- --- --- --- --- --- --- ---I V V A G M L L R G A V V P D S A L 1467 1476 1485 1494 1503 CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC --- --- --- --- --- --- --- --- --- --- ---P F N F Q A A Y G L S D Q L A Q A I 1521 1530 1539 1548 AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3' --- --- --- --- --- --- --- --- --- --- ---S D H Y P V E V M L K *

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FIGURE 14 (A) PAS102

1566 bp mRNA PRI 06-MAR-1995 PAS102.DNA Humanised HMFG1 Fab'2 fused to human DNase I (pAS102) DEFINITION ACCESSION NTD DNase I. KEYWORDS DNase I sequence is from assembled oligos (thus modified c/f SOURCE MHDNASE1.dna) (see Figure 2) ORGANISM Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L. **AUTHORS** Recombinant human DNase I reduces the viscosity of cystic fibrosis TITLE Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990) **JOURNAL** 91067672 MEDLINE 440 q 312 t 469 c BASE COUNT 345 a ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGGAGCGGC 781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC 841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG 901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA 961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC 1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT 1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC 1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC 1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC 1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCTCC 1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCGACAGC 1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG 1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACTTCCA GGCTGCCTAT 1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG 1561 AAGTGA

//

Figure 14 (B)

CUS	EDDNASE10	2 1566 BP	SS-DNA	SY	N 23-	MAR-2001
FINITION	- DDMADDIO	2 1000 51	00 51112			
ACCESSION	_					
KEYWORDS	_					
SOURCE	_					
BASE COUNT	- 345 A	468 C	440 G	313 T	0 OTHER	
ORIGIN	242 1	400 C	110 0			
ORIGIN 1	A TCCCATCCA	CCTCTATCAT	ССТСТТСТТС	GTAGCAACAG	CTACAGGTGT	CCACTCCCAG
61	CTCCACCTCC	TCCACTCTCC	GGCAGAGGTG	AAAAAGCCTG	GGGCCTCAGT	GAAGGTGTCC
121	TCCNNCCCTT	CTCCCTACAC	CTTCAGTGCC	TACTGGATAG	AGTGGGTGCG	CCAGGCTCCA
121	CCANACCCCC	TCCACTCCCT	CCGAGAGATT	TTACCTGGAA	GTAATAATTC	TAGATACAAT
241	CACAACTTCA	AGGGCCGAGT	GACAGTCACT	AGAGACACAT	CCACAAACAC	AGCCTACATG
	GAGCTCAGCA			GCCGTCTATT	ACTGTGCAAG	ATCCTACGAC
	TTTGCCTGGT				CAGTCTCCTC	
					GCACCTCTGG	
				CCCGAACCGG		GTGGAACTCA
401 6/1	CCCCCCCTGA	CCACCGCCGT	GCACACCTTC	CCGGCTGTCC	TACAGTCCTC	AGGACTCTAC
601	TCCCTCACCA	CCGTGGTGAC	CGTGCCCTCC	AGCAGCTTGG	GCACCCAGAC	CTACATCTGC
661	ANCETEDATE	ACAAGCCCAG	CAACACCAAG	GTGGACAAGA	AAGTTGAGCC	CAAATCTTGT
721	CACAAAACTC	ACACATGCTG	TGTCGAGTGT	CCACCGTGTC	CAGCACCAGA	GGGGAGCGGC
10 721 50 781	CCCCTCAACA	TCGCAGCCTT	CAACATCCAG	ACATTTGGGG	AGACCAAGAT	GTCCAATGCC
9/1	ACCCTCGTCA	GCTACATTGT	GCAGATCCTG	AGCCGCTACG	ACATCGCCCT	GGTCCAGGAG
	GTCAGAGACA			AAGCTGCTGG	ACAACCTCAA	TCAGGACGCA
961	CCAGACACCT	ATCACTACGT			GGAACAGCTA	
1021	TACCTGTTCG	TGTACAGGCC	TGACCAGGTG	TCTGCGGTGG	ACAGCTACTA	CTACGATGAT
1021	GGCTGCGAGC	CCTGCGGGAA	CGACACCTTC	AACCGAGAGC	CAGCCATTGT	CAGGTTCTTC
1141	TCCCGGTTCA	CAGAGGTCAG	GGAGTTTGCC	ATTGTTCCCC	TGCATGCGGC	CCCGGGGGAC
1201	GCAGTAGCCG	AGATCGACGC	TCTCTATGAC	GTCTACCTGG	ATGTCCAAGA	GAAATGGGGC
1261		TCATGTTGAT	GGGCGACTTC	AATGCGGGCT	GCAGCTATGT	GAGACCCTCC
		CCATCCGCCT			AGTGGCTGAT	
					GGATCGTGGT	
1441	CTGCTCCGAG	GGGCCGTTGT	TCCCGACTCG	GCTCTTCCCT	TTAACTTCCA	GGCTGCCTAT
1501	GGCCTGAGTG	ACCAACTGGC	CCAAGCCATC	AGTGACCACT	ATCCAGTGGA	GGTGATGCTG
	AAGTGA					
1.7						

1561 GTGATGCTGA AGTGA

Figure 14 (0)

```
SYN
                                                              29-AUG-2000
                       1575 BP SS-DNA
           FDDNASE302
LOCUS
DEFINITION
                                 pAS302
ACCESSION
KEYWORDS
SOURCE
                    Location/Qualifiers
FEATURES
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     frag
                    /note="1 to 1566 of FdDNase102correct"
                               442 G
                                           313 T 0 OTHER
                       474 C
BASE COUNT
                346 A
ORIGIN
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       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
1,0
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG
      781 GGGAGCGGCG GGCTGAAGAT CGCAGCCTTC AACATCCAGA CATTTGGGGA GACCAAGATG
      841 TCCAATGCCA CCCTCGTCAG CTACATTGTG CAGATCCTGA GCCGCTACGA CATCGCCCTG
      901 GTCCAGGAGG TCAGAGACAG CCACCTGACT GCCGTGGGGA AGCTGCTGGA CAACCTCAAT
      961 CAGGACGCAC CAGACACCTA TCACTACGTG GTCAGTGAGC CACTGGGACG GAACAGCTAT
     1021 AAGGAGCGCT ACCTGTTCGT GTACAGGCCT GACCAGGTGT CTGCGGTGGA CAGCTACTAC
     1081 TACGATGATG GCTGCGAGCC CTGCGGGAAC GACACCTTCA ACCGAGAGCC AGCCATTGTC
     1141 AGGTTCTTCT CCCGGTTCAC AGAGGTCAGG GAGTTTGCCA TTGTTCCCCT GCATGCGGCC
     1201 CCGGGGGACG CAGTAGCCGA GATCGACGCT CTCTATGACG TCTACCTGGA TGTCCAAGAG
     1261 AAATGGGGCT TGGAGGACGT CATGTTGATG GGCGACTTCA ATGCGGGCTG CAGCTATGTG
     1321 AGACCCTCCC AGTGGTCATC CATCCGCCTG TGGACAAGCC CCACCTTCCA GTGGCTGATC
     1381 CCCGACAGCG CTGACACCAC AGCTACACCC ACGCACTGTG CCTATGACAG GATCGTGGTT
     1441 GCAGGGATGC TGCTCCGAGG GGCCGTTGTT CCCGACTCGG CTCTTCCCTT TAACTTCCAG
     1501 GCTGCCTATG GCCTGAGTGA CCAACTGGCC CAAGCCATCA GTGACCACTA TCCAGTGGAG
```

' File : PAS102.DNA Range : 1 - 1566 Mode : Normal Codon Table : Universal

FIGURE 14 (D)

, 10)				
5′	ATG (GGA	-	AGC	TGT					TTG	GTA		ACA	GCT		GGT	GTC	54 CAC
	M	G	W	S	С	I	I	L	F	L	V	А	T	A	Υ	G	V	Н
	TCC	CAG	63 GTG	CAG	CTG	72 GTG	CAG	тст	81 GGG	GCA	GAG	90 GTG	AAA	AAG	99 CCT	GGG	GCC	108 TCA
	S	Q	v	Q	L	ν	Q	S	G	Α	E	V	K	K	P	G	A	S
	GTG	AAG	117 GTG	TCC	TGC	126 AAG	GCT	TCT	135 GGC		ACC	144 TTC	AGT	GCC	153 TAC	TGG	ATA	162 GAG
	v		v	 S	C	к		 S	G	Y	T	F	s	Α	Υ	W	ı	E
	TGG	GTG	171 CGC	CAG	GCT	180 CCA	GGA	AAG	189 GGC	CTC	GAG	198 TGG	GTC	GGA	207 GAG	ATT	TTA	216 CCT
	W	V	 R	Q	Α	P	G	К	G	L	Е	w	v	G	Е	I	 L	P
	GGA	AGT	225 AAT	TAA	TCT	234 AGA	TAC	AAT	243 GAG		TTC	252 AAG	GGC	CGA	261 GTG	ACA	GTC	270 ACT
	G	s	N	N	s	R	Y	N	E	K	F	K	G	R	٧	Т	V	${f T}$
	AGA	GAC	279 ACA		ACA	288 AAC		GCC	297 TAC		GAG	306 CTC		AGC	315 CTG		TCI	324 GAG
	 R	D	Т	 S	Т		 Т		Y	M	 E	L	s		 L	R	S	E
	GAC	ACA	333 4 GCC		TAT :	342 TAC		GCA	351 AGA		TAC			, GCC	369 TGG		GC1	378 TAC
	D	Т	Α	V	Y	Y	C	Α	R	S	Y	D	F	A	W	F	A	Y
	TGG	GG(387 C CA	A GG(GTC			TCC				: ACC	423 AAG	GGC	C CCA	432 A TCG
	W	G	Q		т							Α	S	Т	K			S
	GTC	TT	44) C CC				TCC			G AG		468 C TCT	r GG(GC(486 CTG
	V	 F	 P	 L		P						 S						
	GG(C TG	49 C CT		C AA	504 G GA	-	C TT	C CC	C GA	A CC		G AC	G GT			G AA	540 C TCA
	 G	 C		v	 K	 D	 У	 F	 P		 P			 V	 S	 W	 N	S
	GG			G AC			C GT			C TT			T GT			G TC		594 A GGA
																		 G

CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAGC L Y S L S S V V T V P S S S L G T Q 657 666 675 684 693 702 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAA AAA T Y I C N V N H K P S N T K V D K K 711 720 729 738 747 756 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCC V E P K S C D K T H T C C V E C P P TGC CCA GCA CCT GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAC TGC CCA GCA CCT GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAC TGC CCA GCA CCT GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAC TGC CCA GCA CCT GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAC	_
657 666 675 684 693 702 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA T Y I C N V N H K P S N T K V D K K 711 720 729 738 747 756 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCC V E P K S C D K T H T C C V E C P P 765 774 783 792 801 816	
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA T Y I C N V N H K P S N T K V D K K 711 720 729 738 747 756 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCC V E P K S C D K T H T C C V E C P P 765 774 783 792 801 810	
711 720 729 738 747 756 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCC V E P K S C D K T H T C C V E C P P 765 774 783 792 801 810	
711 720 729 738 747 756 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCC V E P K S C D K T H T C C V E C P P 765 774 783 792 801 810	-
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCC V E P K S C D K T H T C C V E C P P 765 774 783 792 801 810	
V E P K S C D K T H T C C V E C P P 765 774 783 792 801 810	
765 774 783 792 801 810	3
The state of the s	
TGC CCA GCA CCT GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAC	
	3
C P A P E G S G G L K I A A F N I Q	
819 828 837 846 855 866 ACA TTT GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CA	
	-
T F G E T K M S N A T L V S Y I V Q	
873 882 891 900 909 91	
ATC CTG AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CT	G -
I L S R Y D I A L V Q E V R D S H L	
927 936 945 954 963 97	
ACT GCC GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TA	T
T A V G K L L D N L N Q D A P D T Y	
981 990 999 1008 1017 102	6
CAC TAC GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CT	`G
H Y V V S E P L G R N S Y K E R Y I	٠-
1035 1044 1053 1062 1071 108	30
TTC GTG TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GA	
F V Y R P D Q V S A V D S Y Y Y D I	
1089 1098 1107 1116 1125 113	
GGC TGC GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AC	3G
G C E P C G N D T F N R E P A I V	R
1143 1152 1161 1170 1179 11 TTC TTC TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT G	
F F S R F T E V R E F A I V P L H	
1197 1206 1215 1224 1233 12	

GCC CCG GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---P G D A V A E I D A L Y D V Y L D 1251 1260 1269 1278 1287 1296 GTC CAA GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG ___ __ __ __ __ __ __ __ __ __ __ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ V Q E K W G L E D V M L M G D 1305 1314 1323 1332 1341 1350 GGC TGC AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC G C S Y V R P S Q W S S I R 1359 1368 1377 1386 1395 CCC ACC TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG ___ ___ __ __ __ __ __ __ __ __ __ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ P T F Q W L I P D S A D T 1413 1422 1431 1440 1449 1458 CAC TGT GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT H C A Y D R I V V A G M L L R G A V 1467 1476 1485 1494 1503 1512 GTT CCC GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC ___ ___ __ __ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ V P D S A L P F N F Q A A Y G L S D 1530 1539 1548 1557 1521 CAA CTG GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'

FIGURE IS

(A) pAS103

06-MAR-1995 1560 bp mRNA PAS103.DNA LOCUS DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS103) ACCESSION NID DNase I. KEYWORDS DNase I sequence is from assembled oligos (thus modified c/f SOURCE MHDNASE1.dna) ORGANISM Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L. **AUTHORS** Recombinant human DNase I reduces the viscosity of cystic fibrosis TITLE Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990) **JOURNAL** MEDLINE 91067672 BASE COUNT 344 a 468 c 436 q 312 t ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGCGGGCTG 781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC 841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA 901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC 961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG 1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC 1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG 1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA 1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG 1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG 1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC 1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC 1441 CGAGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG 1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA

//

1

Figure 15 (B)

```
SYN
                                                              25-AUG-2000
                         1560 BP SS-DNA
            FDDNASE103
TOCUS
FINITION
CCESSION
KEYWORDS
SOURCE
                     Location/Qualifiers
FEATURES
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     frag
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                                           313 T
BASE COUNT
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      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
Oil
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
B.C.
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGCGGGCTG
      781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
      841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
      901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
      961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
     1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
     1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
     1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
      1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
     1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
      1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
     1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
     1441 CGAGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
     1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA
```

1561 CTGAAGTGA

Figure 15 (c)

```
29-AUG-2000
                                                    SYN
                        1569 BP SS-DNA
           FDDNASE103
LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
                     Location/Qualifiers
FEATURES
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     frag
                     /note="1 to 1560 of FdDNase103correct"
                     join(10..>729,<802..1569)
     frag
                     /note="1 to 1560 of PAS103.dna [Split]"
                     730..801
     frag
                     /note="1 to 72 of 103/107linker"
                     join(730..>780,<781..801)
     frag
                     /note="1 to 78 of 102linker [Split]"
                                           313 T
                         473 C
                                  438 G
BASE COUNT
                345 A
ORIGIN
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
     . 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG
      781 GGCGGGCTGA AGATCGCAGC CTTCAACATC CAGACATTTG GGGAGACCAA GATGTCCAAT
      841 GCCACCCTCG TCAGCTACAT TGTGCAGATC CTGAGCCGCT ACGACATCGC CCTGGTCCAG
      901 GAGGTCAGAG ACAGCCACCT GACTGCCGTG GGGAAGCTGC TGGACAACCT CAATCAGGAC
      961 GCACCAGACA CCTATCACTA CGTGGTCAGT GAGCCACTGG GACGGAACAG CTATAAGGAG
     1021 CGCTACCTGT TCGTGTACAG GCCTGACCAG GTGTCTGCGG TGGACAGCTA CTACTACGAT
     1081 GATGGCTGCG AGCCCTGCGG GAACGACACC TTCAACCGAG AGCCAGCCAT TGTCAGGTTC
     1141 TTCTCCCGGT TCACAGAGGT CAGGGAGTTT GCCATTGTTC CCCTGCATGC GGCCCCGGGG
     1201 GACGCAGTAG CCGAGATCGA CGCTCTCTAT GACGTCTACC TGGATGTCCA AGAGAAATGG
     1261 GGCTTGGAGG ACGTCATGTT GATGGGCGAC TTCAATGCGG GCTGCAGCTA TGTGAGACCC
     1321 TCCCAGTGGT CATCCATCCG CCTGTGGACA AGCCCCACCT TCCAGTGGCT GATCCCCGAC
     1381 AGCGCTGACA CCACAGCTAC ACCCACGCAC TGTGCCTATG ACAGGATCGT GGTTGCAGGG
     1441 ATGCTGCTCC GAGGGGCCGT TGTTCCCGAC TCGGCTCTTC CCTTTAACTT CCAGGCTGCC
     1501 TATGGCCTGA GTGACCAACT GGCCCAAGCC ATCAGTGACC ACTATCCAGT GGAGGTGATG
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File: PAS103.DNA Range: 1 - 1560 Codon Table: Universal

5′

Mode : Normal

FIGURE 15(D)

ΔTΓC	GG N	TGC		GC '	тст	18 ATC			27 TTC	TTG			36 3CA	ACA	GCT	45 ACA	GGT	GTC		54 AC
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rcc	CAG	6.3 GTV		'AC	CTG	72 GTG			81 GGG		. GA		90 GTG	AAA	AAG	99 CCT	GGG	GCC		08 CA
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S	Q	V		Q	L	V	Q	S	G	A	E	3	V	K	K	P	G	Α		S
		11				126							144	3 O(0)	000	153		- 7. m 7		62
GTG	AAG	GT	G 7	rcc 	TGC	AAG	GCT		GGC	TAC	: A(AGT						
v	K	V		S	С	K	A	s	G	Y	•	r	F	S	A	Y	W	I		E
		17				180			189				198							16
TGG	GTG	CG	C (CAG	GCT	CCA	GGA	AAG	GGC	CTO	G G	AG 	TGG	GTC	GGA	GAC	TTA	TT?		:C:
W	V	R	l.	Q	A	P	G	ĸ	G	L		E	W	V	G	E	1	L		P
		22				234							252							27
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TG	G GG	C C	AA	GGG	AC:	r CT	G GT	C AC	A GT	C TO	CC :	TCA	GCC	TC	C AC	C AA	.G GG	C CC	A	TC
W			Q Q	G	Т	 L	 V	T	, A		5	s	Α	S	г	' K		i I		5
		4	41			45	0		45	9			46	8		47	7			48
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639 603 612 621 630 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG L Y S L S S V V T V P S S S L G T O 675 684 693 657 666 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA T Y I C N V N H K P S N T K V D K K 729 738 747 720 711 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG V E P K S C D K T H T C C V E C P P 792 774 783 TGC CCA GCA CCT GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT PAPEGGLKIAAFN 819 828 837 846 855 GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG G E T K M S N A T L V S Y I V Q I L 891 900 909 873 882 AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC S R Y D I A L V Q E V R D S H L T A 927 936 945 954 963 GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC --- --- --- --- --- --- --- --- --- --- --- --- ---V G K L L D N L N Q D A P D T Y H Y 990 999 1008 1017 GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG V S E P L G R N S Y K E R Y L F 1062 1071 1080 1044 1053 1035 TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC Y R P D O V S A V D S Y Y Y D D G C 1089 1098 1107 1116 1125 GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC E P C G N D T F N R E P A I V R F F 1143 1152 1161 1170 1179 TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG S R F T E V R E F A I V P L H A A P 1197 1206 1215 1224 1233 1242

GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA --- --- --- --- --- --- --- --- --- --- --- --- ---1251 1260 1269 1278 1287 1296 GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC ___ ___ E K W G L E D V M L M G D F N A G C 1305 1314 1323 1332 1341 AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC _______ S Y V R P S Q W S S I R L W T S P T 1359 1368 1377 1386 1395 1404 TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT ___ ___ __ __ __ __ __ __ __ __ __ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ F Q W L I P D S A D T T A T P T H C 1413 1422 1431 1440 1449 GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC A Y D R I V V A G M L L R G A V V P 1476 1485 1494 1503 1512 1467 GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG ___ ___ 1530 1539 1548 1557 1521 GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3' A Q A I S D H Y P V E V M L K *

FIGURE 16

(h) pAS104

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06-MAR-1995
                         1560 bp
                                    mRNA
                                                     PRI
            PAS104.DNA
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS104)
Position 924 G to A by ggg to gag
Linker GR instead of GG (position 777)
ACCESSION
NTD
KEYWORDS
            DNase I.
            DNase I sequence is from assembled oligos (thus modified c/f
SOURCE
MHDNASE1.dna)
  ORGANISM Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
  AUTHORS
            Recombinant human DNase I reduces the viscosity of cystic fibrosis
  TITLE
            Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
  JOURNAL
            91067672
  MEDLINE
                                   434 g
                                            312 t
                346 a
                          468 c
BASE COUNT
ORIGIN
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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGCAGGCTG 781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC 841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA 901 GACAGCCACC TGACTGCCGT GGAGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC 961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG 1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC 1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG 1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA 1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG 1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG 1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC 1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC 1441 CGAGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG 1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA

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. Figure 16(B)

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SYN
                                                              25-AUG-2000
                         1560 BP SS-DNA
            FDDNASE104
CUS
DEFINITION
"CCESSION
***CYWORDS
SOURCE
                     Location/Qualifiers
FEATURES
                     join(1..>720,<793..1560)
     fraq
                     /note="1 to 1560 of PAS104.dna [Split]"
                     721..792
     frag
                     /note="1 to 72 of 104linker"
                     join(721..>774,<776..792)
     fraq
                     /note="1 to 72 of 103linker [Split]"
                     join(721..>771,<772..>774,<776..792)
     frag
                     /note="1 to 78 of 102linker [Split]"
                                           313 T
                                                      0 OTHER
                         467 C
                                  434 G
                346 A
BASE COUNT
ORIGIN
        1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
179
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
(13)
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
NE.
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGCAGGCTG
      781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
      841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
      901 GACAGCCACC TGACTGCCGT GGAGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
      961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
     1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
     1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
     1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
     1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
     1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
     1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
     1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
     1441 CGAGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
     1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA
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		GTG		117 GTG	TCC		126 AAG	GCT	TCT	135 GGC	TAC	ACC	144 TTC	AGT	GCC	153 TAC	TGG	ATA	
		 V	 K	 V	 s	 C	 K	 A	 S	 G	 У	 Т	 F	s	A	Y	w		E
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•		TGG	GTG		CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT	TTA	CCT
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1		AGA	GAC	279 ACA		ACA	288 AAC	ACA	GCC	297 TAC		GAG	306 CTC		AGC	315 CTG		TCT	324 GAG
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200 2000 20 2000 20 2000 20 2000 20 2000 20 2000		GAC	ACA			TAT			' GCA	AGA	TCC		GAC		GCC			GCT	TAC
		D	Т	Α	V	Υ	Y	С	A	R			D	F	A	W	F	Α	Y
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		GG	C TG	49 C CT		C AA	50 G GA		С ТТ		C GA	A CC	G GT	G AC	G GT			G AA	C TCA
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CTC	TAC	TCC		AGC	AGC			ACC		. –									-
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ACC	TAC	ATC	TGC	AAC	GTG	TAA	CAC	AAG	CCC	A :	.GC	AAC	ACC	AAG	GTG	GAC	AAG	A.A 	.A
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		711			720			729				738			747			75	
GTT	GAG	CCC	LAA :	A TC	r TGT	GAC	AAA	ACT	CA	C A	ACA	TGC	TGT	GTG	GAG	TGC	CCA	. CC	CG
v	E	P	K	s	С	D	К	т	Н		Т	С	С	V	E	С	P	I	2
		769			774	•						792							10
TGC	CCA	. GC	A CC	r ga	A GG(AGG	CTC	AAG	TA :	C (GCA	GCC	TTC	AAC	ATC	CAG	ACA	T'	PT
С	P	A	P	E	G	R	L	K	I		A	A	F	N	I	Q	Т	1	F
GGG	GAG	81 AC		G AT	829 G TC		r GC(831 AC		c (GTC	846 AGC		TTA	855 GTG)TA		64 TG
G	E	Т	K	M	ı s	N	A	т	I	,	V	S	Y	Ι	V	Q	Ι		L
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V	V	′ :	S	E	P I	. (; F	1 5	1	S	Y	K	Е	R	Y	L	F		V
		10																	
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G <i>P</i>	G C	10 CC T	89 GC G	GG F	10 AC G	98 AC A	CC T	11 TC A	07 AC (GA	. GA	111 G CC	6 agc	C AT	112 T G1	25 CC AC	G T	1 rc	134 TTC
H	Ξ :	P	С	G	N	D '	r	F.	N	К	E	P	, 4	7 7	. \	/ r		r	Г
T	CC C	GG 1	TC A	ACA (11 GAG G	TC A	GG G	AG T	TT	GCC	TA	T GI	T CC	CC CI	rg ca	AT GO	CG G	1 CC	188 CCG
- :	 S				 E												A .		
		1	197		12	:06		12	:15			122	24		12	33		1	242

GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA --- --- --- --- --- --- --- --- --- --- --- ---1260 1269 1278 1287 1296 1251 GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC --- --- --- --- --- --- --- --- --- --- --- --- --- ---E K W G L E D V M L M G D F N A G C 1305 1314 1323 1332 1341 1350 AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC --- --- --- --- --- --- --- --- --- --- --- --- ---S Y V R P S Q W S S I R L W T S P T 1386 1395 1404 1368 1377 1359 TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT ___ ___ 1440 1449 1458 1413 1422 1431 GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC 1476 1485 1494 1503 1512 1467 GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG --- --- --- --- --- --- --- --- --- --- --- --- ---1521 1530 1539 1548 1557 GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3' --- --- --- --- --- --- --- --- --- --- --- --- ---A Q A I S D H Y P V E V M L K *

L

11

FIGURE 17

(A) pAS105

06-MAR-1995 PRI 1578 bp mRNA LOCUS DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40 NLS(pAS105) ACCESSION NID DNase I. KEYWORDS DNase I sequence is from assembled oligos (thus modified c/f SOURCE MHDNASE1.dna) ORGANISM Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L. AUTHORS Recombinant human DNase I reduces the viscosity of cystic fibrosis TITLE sputum Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990) JOURNAL 91067672 MEDLINE 442 g 310 t 353 a 473 c BASE COUNT ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAG GCGCCTGAA GATCGCAGCC 781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT 841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG 901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC 961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG 1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG 1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC 1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC CGAGATCGAC 1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG 1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC 1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA 1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT 1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG

1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGGGGGG CGGACCCAAA

> NLS

1561 AAGAAGCGCA AGGTTTGA



Figure 17(B)

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FINITION
ACCESSION
MYWORDS
SOURCE
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                                  443 G
                          471 C
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       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
    : 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
1. . .
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
83
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
\mathbb{S} \subseteq \mathbb{R}
       601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
       661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
       721 GACAAAACTC ACACATGTCC ACCGTGTCCA GCACCAGAGG GCGGGCTGAA GATCGCAGCC
       781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT
       841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
       901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
      961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
      1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
      1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC
      1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC CGAGATCGAC
      1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
      1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC
      1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
      1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
      1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
      1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGGGGGG CGGACCCAAA
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1561 AAGAAGCGCA AGGTTTGA

rigure 17k)

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                        1587 BP SS-DNA
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DEFINITION
ACCESSION
EEYWORDS
SOURCE
                     Location/Qualifiers
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     frag
                     /note="1 to 80 of 102linker [Split]"
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                         477 C
BASE COUNT
                354 A
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       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
     421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG CGGGCTGAAG
      781 ATCGCAGCCT TCAACATCCA GACATTTGGG GAGACCAAGA TGTCCAATGC CACCCTCGTC
      841 AGCTACATTG TGCAGATCCT GAGCCGCTAC GACATCGCCC TGGTCCAGGA GGTCAGAGAC
      901 AGCCACCTGA CTGCCGTGGG GAAGCTGCTG GACAACCTCA ATCAGGACGC ACCAGACACC
      961 TATCACTACG TGGTCAGTGA GCCACTGGGA CGGAACAGCT ATAAGGAGCG CTACCTGTTC
     1021 GTGTACAGGC CTGACCAGGT GTCTGCGGTG GACAGCTACT ACTACGATGA TGGCTGCGAG
     1081 CCCTGCGGGA ACGACACCTT CAACCGAGAG CCAGCCATTG TCAGGTTCTT CTCCCGGTTC
     1141 ACAGAGGTCA GGGAGTTTGC CATTGTTCCC CTGCATGCGG CCCCGGGGGA CGCAGTAGCC
     1201 GAGATCGACG CTCTCTATGA CGTCTACCTG GATGTCCAAG AGAAATGGGG CTTGGAGGAC
     1261 GTCATGTTGA TGGGCGACTT CAATGCGGGC TGCAGCTATG TGAGACCCTC CCAGTGGTCA
      1321 TCCATCCGCC TGTGGACAAG CCCCACCTTC CAGTGGCTGA TCCCCGACAG CGCTGACACC
      1381 ACAGCTACAC CCACGCACTG TGCCTATGAC AGGATCGTGG TTGCAGGGAT GCTGCTCCGA
      1441 GGGGCCGTTG TTCCCGACTC GGCTCTTCCC TTTAACTTCC AGGCTGCCTA TGGCCTGAGT
      1501 GACCAACTGG CCCAAGCCAT CAGTGACCAC TATCCAGTGG AGGTGATGCT GAAGGGGGGC
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1561 GGACCCAAAA AGAAGCGCAA GGTTTGA

. File: PAS105.DNA Range: 1 - 1578 Mode: Normal Codon Table: Universal

FIGURE 17 (D)

												r		Ch.	12		/
ATG '	GGA	9 TGG	AGC	TGT	18 ATC	ATC	CTC	27 TTC	TTG	GTA	36 GCA	ACA	GCT	45 ACA	GGT	GTC	54 CAC
 М	 G	W	 S	C	I	1	L L	F	L	v	A	Т	Α	Т	G	V	Н
TCC	CAG	63 GTG	CAG	CTG	72 GTG	CAG	TCT	81 GGG	GCA	GAG	90 GTG	AAA	AAG	99 CCT	GGG	GCC	108 TCA
 S	 Q	 V	 Q	 L	 V	 Q	s	G	 A	 E	v		к	P	 G	 А	s
GTG	AAG	117 GTG	TCC	TGC	126 AAG	GCT	TCT	135 GGC		ACC	144 TTC		GCC	153 TAC	TGG	ATA	162 GAG
v	 K	 V	 S		 к	 A	 s		 Y	 T	 F	 S	 A	Y	W	 I	E
TGG	GTG	171 CGC		GCT	180 CCA		AAG	GGC	CTC		TGG	GTC	GGA	207 GAG		TTA	216 CCT
W	v	R	Q	Α	P	G	K	G		E	W	v	G	E	I	L	P
GGA	AGT	225 ` AAT		TCI	234 ` AGA		raa :			TTC			CGA	261 GTG		GTC	270 ACT
G	s	N	N	s	R	Y	N	E	K	F	K	G	R	V	Т	V	Т
AGA	GAC	279 ACA		C ACA	288 AAC		A GCC	297 TAC		GAC	306 G CTC		C AGO	315 C CTC		TC1	324 GAG
 R	 D	Т	s	Т	N	T	 A	Y	м	 E	L	 S	S	L	 R	S	E
GAC	: AC	33: A GC(C TA	342 TAC		r GC	35: A AG		C TA	360 C GA0		r GC0	369 TG0		r GC'	378 r TAC
D	T	A	 V	Y	· У	 C	A	R	 S	 Y	D	 F	Α	W	 F	Α	Y
TGC	G GG	38 C CA		G AC	39 T CT		C AC	40 A GT		с тс	41 A GC		C AC	42 C AA		c cc	432 A TCG
W	 G	 Q					 T				 A						 S
GT(с тт	44 C CC	C CI			СТС		C AA	G AG			T GG			A GC		486 C CTC
 V	 F			 A													
GG [,]			G G			C TA		rc cc	CC GA	A CO		G AC	G GI	G TC	G TO		C TC
G				 J F												1 1	
GG	C G	54 CC C		CC AG		GC G1		AC AC	CC T		CG GC	CT G	rc c:			CC TO	594 CA GG
	; ;	A		 T :			J I						J 3	. () :	5 :	5 G

- } -

621 630 639 612 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG 684 675 666 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA ___ ___ T Y I C N V N H K P S N T K V D K K 756 729 738 720 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT --- --- --- --- --- --- --- --- --- --- --- --- ---V E P K S C D K T H T C P P C P A P 792 783 774 GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG --- --- --- --- --- --- --- --- --- --- --- --- ---E G G L K I A A F N I Q T F G E T K 837 846 819 828 ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC $\begin{smallmatrix} M & S & N & A & T & L & V & S & Y & I & V & Q & I & L \\ \end{smallmatrix}$ 900 909 891 882 873 ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG ___ ___ ___ ___ ___ ___ I A L V Q E V R D S H L T A V G K L 945 954 963 936 CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG 990 999 1008 1017 CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC --- --- --- --- --- --- --- --- --- --- --- ---L G R N S Y K E R Y L F V Y R P D 1035 1044 1053 1062 1071 1080 CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---Q V S A V D S Y Y Y D D G C E P C G 1116 1107 1125 1098 AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA ___ ___ N D T F N R E P A I V R F F S R 1152 1161 1170 1179 GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA ___ ___ 1197 1206 1215 1224 1233 1242

R K V *

GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC EIDALYDVYLDVQEKWG 1251 1260 1269 1278 1287 1296 TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA --- --- --- --- --- --- --- --- --- --- --- --- ---L E D V M L M G D F N A G C S Y V R 1305 1314 1323 1332 1341 1350 CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG --- --- --- --- --- --- --- --- --- --- --- --- ---PSQWSSIRLWTSPTFQWL 1359 1368 1377 1386 1395 1404 ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG --- --- --- --- --- --- --- --- --- --- --- --- ---I P D S A D T T A T P T H C A Y D R 1413 1422 1431 1440 1449 1458 ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT ___ ___ I V V A G M L L R G A V V P D S A L 1467 1476 1485 1494 1503 1512 CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC PFNFQAAYGLSDQLAQAI 1521 1530 1539 1548 1557 1566 AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG S D H Y P V E V M L K G G G P K K K 1575 CGC AAG GTT TGA 3'

FIGURE 18

/A) pAS106

PRI 1596 bp mRNA LOCUS PAS106.DNA DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40 NLS(pAS106) ACCESSION NTD KEYWORDS DNase I. DNase I sequence is from assembled oligos (thus modified c/fSOURCE MHDNASE1.dna) ORGANISM Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L. AUTHORS Recombinant human DNase I reduces the viscosity of cystic fibrosis TITLE sputum Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990) **JOURNAL** 91067672 MEDLINE BASE COUNT 355 a 475 c 452 g 314 t ORIGIN

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61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACA<mark>TGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGGAGCGGC</mark>
781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC 841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG 901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA 961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC 1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT 1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC 1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC 1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC 1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCTCC 1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCGACAGC 1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG 1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACTTCCA GGCTGCCTAT 1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG 1561 AAGGGGGCG GACCCAAAAA GAAGCGCAAG GTTTGA

- NLS

Figure 12(3)

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FEYWORDS
COURCE
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       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
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    # 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
    :541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
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      901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
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     1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
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     1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCGACAGC
     1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
     1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACTTCCA GGCTGCCTAT
     1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
     1561 AAGGGGGCG GACCCAAAAA GAAGCGCAAG GTTTGA
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Figure 12(c)

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           FDDNASE106
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YWCRDS
SOURCE
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FEATURES
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       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
     · 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG
      781 GGGAGCGGCG GGCTGAAGAT CGCAGCCTTC AACATCCAGA CATTTGGGGA GACCAAGATG
      841 TCCAATGCCA CCCTCGTCAG CTACATTGTG CAGATCCTGA GCCGCTACGA CATCGCCCTG
      901 GTCCAGGAGG TCAGAGACAG CCACCTGACT GCCGTGGGGA AGCTGCTGGA CAACCTCAAT
      961 CAGGACGCAC CAGACACCTA TCACTACGTG GTCAGTGAGC CACTGGGACG GAACAGCTAT
     1021 AAGGAGCGCT ACCTGTTCGT GTACAGGCCT GACCAGGTGT CTGCGGTGGA CAGCTACTAC
     1081 TACGATGATG GCTGCGAGCC CTGCGGGAAC GACACCTTCA ACCGAGAGCC AGCCATTGTC
     1141 AGGTTCTTCT CCCGGTTCAC AGAGGTCAGG GAGTTTGCCA TTGTTCCCCT GCATGCGGCC
     1201 CCGGGGGACG CAGTAGCCGA GATCGACGCT CTCTATGACG TCTACCTGGA TGTCCAAGAG
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      1501 GCTGCCTATG GCCTGAGTGA CCAACTGGCC CAAGCCATCA GTGACCACTA TCCAGTGGAG
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1596 Mode : Normal FIGURE 18(D) Codon Table : Universal 27 18 9 ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC --- --- --- --- --- --- --- --- --- --- --- --- --- --- $\begin{smallmatrix} M & G & W & S & C & I & I & L & F & L & V & A & T & A & T & G & V & H \\ \end{smallmatrix}$ 72 81 90 TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---S Q V Q L V Q S G A E V K K P G A 144 135 126 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---V K V S C K A S G Y T F S A 198 207 189 180 TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT --- --- --- --- --- --- --- --- --- --- --- --- ---W V R Q A P G K G L E W V G E I L P 252 261 243 234 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---G S N N S R Y N E K F K G R V T V T 306 315 297 279 288 AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG Y M E L S S L R S E R D T S T N T A 360 369 351 342 333 GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC R S Y D F A W F A Y 396 405 414 423 387 TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---468 477 459 450 441 GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG --- --- --- --- --- --- --- --- --- ---V F P L A P S S K S T S G G T 522 531 513 504 495 GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA G C L V K D Y F P E P V T V S W N S 567 576 585 558 GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA

630 639 612 621 603 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG L Y S L S S V V T V P S S S L G T Q 693 675 684 666 657 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA ___ ___ ___ T Y I C N V N H K P S N T K V D K K 747 720 729 738 711 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG --- --- --- --- --- --- --- --- --- --- ---783 792 801 774 765 TGC CCA GCA CCT GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG --- --- --- --- --- --- --- --- --- --- --- --- --- ---PAPEGSGGLKIAAFNIQ 846 855 837 828 819 ACA TTT GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG --- --- --- --- --- --- --- --- --- --- --- --- --- ---T F G E T K M S N A T L V S Y I V Q 909 900 882 891 873 ATC CTG AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG I L S R Y D I A L V Q E V R D S H L 945 954 963 936 ACT GCC GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT --- --- --- --- --- --- --- --- --- --- --- --- --- ---999 1008 1017 990 CAC TAC GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG --- --- --- --- --- --- --- --- --- --- --- --- ---H Y V V S E P L G R N S Y K E R Y L 1053 1062 1071 1080 1044 1035 TTC GTG TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT --- --- --- --- --- --- --- --- --- --- --- --- --- --- $\begin{smallmatrix} F & V & Y & R & P & D & Q & V & S & A & V & D & S & Y & Y & D & D \end{smallmatrix}$ 1098 1107 1116 1125 GGC TGC GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG G C E P C G N D T F N R E P A I V R 1143 1152 1161 1170 1179 1188 TTC TTC TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG F F S R F T E V R E F A I V P L H A 1197 1206 1215 1224 1233 1242 GCC CCG GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT A P G D A V A E I D A L Y D V Y 1251 1260 1269 1278 1287 1296 GTC CAA GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG V Q E K W G L E D V M L M G D F N A 1314 1323 1332 1341 GGC TGC AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC G C S Y V R P S Q W S S I R L W T S 1368 1377 1386 1395 1359 CCC ACC TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG P T F Q W L I P D S A D T T A T P T 1422 1431 1440 1449 1458 1413 CAC TGT GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT H C A Y D R I V V A G M L L R G A V 1467 1476 1485 1494 1503 1512 GTT CCC GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC 1530 1539 1548 1557 1566 CAA CTG GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG Q L A Q A I S D H Y P V E V M L K G 1575 1584 1593 GGC GGA CCC AAA AAG AAG CGC AAG GTT TGA 3' ___ ___ ___ ___ G G P K K K R K V

FIGURE 19

(A) pAS107

```
1590 bp
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            PAS107.DNA
                                                     PRI
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40 NLS(pAS107)
ACCESSION
KEYWORDS
            DNase T.
SOURCE
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  ORGANISM Homo sapiens
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            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
  AUTHORS
  TITLE
            Recombinant human DNase I reduces the viscosity of cystic fibrosis
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  JOURNAL
            Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
  MEDLINE
            91067672
BASE COUNT
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LONLS



Figure 19 (8)

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MAYWORDS
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                                  448 G
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      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
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      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
7.7
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
4.
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      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGCGGGCTG
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      841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
      901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
      961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
     1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
     1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
     1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
     1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
     1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
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     1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
     1441 CGAGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
     1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGGGG
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1561 GGCGGACCCA AAAAGAAGCG CAAGGTTTGA

· Figure 19 (C)

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accession	_													
KEYWORDS	_													
SOURCE	_													
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frag		join(10>7	29 < 802 - 15	1991										
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frag		join(730>												
IIag		/note="1 to 78 of 102linker [Split]"												
BASE COUNT	355 A		450 G	315 T	0 OTHER									
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61	CACTCCCAGG	TGCAGCTGGT	GCAGTCTGGG	GCAGAGGTGA	AAAAGCCTGG	GGCCTCAGTG								
121	AAGGTGTCCT	GCAAGGCTTC	TGGCTACACC	TTCAGTGCCT	ACTGGATAGA	GTGGGTGCGC								
181	CAGGCTCCAG	GAAAGGGCCT	CGAGTGGGTC	GGAGAGATTT	TACCTGGAAG	TAATAATTCT								
747 241	AGATACAATG	AGAAGTTCAA	GGGCCGAGTG	ACAGTCACTA	GAGACACATC	CACAAACACA								
301	GCCTACATGG	AGCTCAGCAG	CCTGAGGTCT	GAGGACACAG	CCGTCTATTA	CTGTGCAAGA								
361	TCCTACGACT	TTGCCTGGTT	TGCTTACTGG	GGCCAAGGGA	CTCTGGTCAC	AGTCTCCTCA								
ac 421	GCCTCCACCA	AGGGCCCATC	GGTCTTCCCC	CTGGCACCCT	CCTCCAAGAG	CACCTCTGGG								
9 481	GGCACAGCGG	CCCTGGGCTG	CCTGGTCAAG	GACTACTTCC	CCGAACCGGT	GACGGTGTCG								
541	TGGAACTCAG	GCGCCCTGAC	CAGCGGCGTG	CACACCTTCC	CGGCTGTCCT	ACAGTCCTCA								
601	GGACTCTACT	CCCTCAGCAG	CGTGGTGACC	GTGCCCTCCA	GCAGCTTGGG	CACCCAGACC								
661	TACATCTGCA	ACGTGAATCA	CAAGCCCAGC	AACACCAAGG	TGGACAAGAA	AGTTGAGCCC								
721	AAATCTTGTG	ACAAAACTCA	CACATGCTGT	GTCGAGTGTC	CACCGTGTCC	AGCACCAGAG								
781	GGCGGGCTGA	AGATCGCAGC	CTTCAACATC	CAGACATTTG	GGGAGACCAA	GATGTCCAAT								
841	GCCACCCTCG	TCAGCTACAT	TGTGCAGATC	CTGAGCCGCT	ACGACATCGC	CCTGGTCCAG								
901	GAGGTCAGAG	ACAGCCACCT	GACTGCCGTG	GGGAAGCTGC	TGGACAACCT	CAATCAGGAC								
961	GCACCAGACA	CCTATCACTA	CGTGGTCAGT	GAGCCACTGG	GACGGAACAG	CTATAAGGAG								
1021	CGCTACCTGT	TCGTGTACAG	GCCTGACCAG	GTGTCTGCGG	TGGACAGCTA	CTACTACGAT								
1081	GATGGCTGCG	AGCCCTGCGG	GAACGACACC	TTCAACCGAG	AGCCAGCCAT	TGTCAGGTTC								
1141	TTCTCCCGGT	TCACAGAGGT	CAGGGAGTTT	GCCATTGTTC	CCCTGCATGC	GGCCCCGGGG								
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1261	GGCTTGGAGG	ACGTCATGTT	GATGGGCGAC	TTCAATGCGG	GCTGCAGCTA	TGTGAGACCC								
1321	TCCCAGTGGT	CATCCATCCG	CCTGTGGACA	AGCCCCACCT	TCCAGTGGCT	GATCCCCGAC								
1381	AGCGCTGACA	CCACAGCTAC	ACCCACGCAC	TGTGCCTATG	ACAGGATCGT	GGTTGCAGGG								
1441	ATGCTGCTCC	GAGGGGCCGT	TGTTCCCGAC	TCGGCTCTTC	CCTTTAACTT	CCAGGCTGCC								
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1561 CTGAAGGGGG GCGGACCCAA AAAGAAGCGC AAGGTTTGA

File: PAS107.DNA Range: 1 - 159 Codon Table: Universal 1590

Mode : Normal

FIGURE 19 (0)

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		9			18			27			36			45			54
ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC
M	G	W	S	С	I	I	L	F	L	V	А	T	А	Т	G	V	Н
		63			72			81			90			99			108
TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCA	GAG	GTG	AAA	AAG	CCT	GGG	GCC	TC
S	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S
		117			126			135			144			153			16:
GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GA
v	К	V	s	С	ĸ	A	s	G	Y	т	F	s	~ A	Y	W	I	E
		171			180			189			198			207			21
TGG	GTG	CGC	CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT	TTA	CC
W	v	R	Q	A	P	G	K	G	L	E	W	v	G	E	I	L	P
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GGA	AGT	AAT	TAA	TCT	AGA	TAC	TAA	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	AC
G	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	Т	v	T
		279			288			297			306			315			32
AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GA
R	D	T	S	Т	N	T	A	Y	М	E	L	S	S	L	R	S	E
		333			342			351			360			369			37
GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA	AGA	TCC	TAC	GAC	TTT	GCC	TGG	TTT	GCT	TA
D	Т	Α	V	Y	Y	С	А	R	S	Y	D	F	A	M	F	А	Y
		387			396			405			414			423			43
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W	G	Q	G	Т	L	V	Т	V	S	S	A	S	T	K	G	Р	5
		441			450									477			48
GTC	TTC	CCC	CTG	GCA	ccc			AAG			TCT			ACA	GCG	GCC	
V	F	Р	L	A	P	S	S	ĸ	S	T	S	G	G	Т	А	A	I
		495															54
GGC	TGC				GAC								GTC			AAC	
G	С				D											N	
		549			558				7		576			585			5.5
	CCC	· CTC	2 200	ACC	000	CTC	CAC	2 200	nav.	000	000	conc	Cm	CNC	000		00
GGC								. ACC				. GIC	. CI7	CAC		TCA	

- 1 -

CTC	TAC	603 TCC	CTC		612 AGC	GTG		621 ACC		ccc		AGC		639 TTG	GGC	ACC	648 CAG
 L	 Y	 S	 L	 S	 S	v	v	т	v	 Р	S	 S	s		G	T	Q
ACC	TAC	657 ATC	TGC		666 GTG	TAA	CAC	675 AAG	CCC	AGC	684 AAC	ACC	AAG	693 GTG	GAC	AAG	702 AAA
т	 Y		C	 N	 V	 N		- K	P	 S	 N	 Т	 К	v	D	 K	 K
Cmm	CAC	711 CCC	מממ	ጥርጥ	720 TGT		ΑΑΑ	729 ACT		ACA	738 TGC	TGT	GTG	747 GAG	TGC	CCA	756 CCG
 V	 E	 P	 K	 S	 C	 D	 K	 T	Н		 C			 E	 C	 P	 P
		765			774	~~~	ama	783	3.000	CCA	792	mm/C	220	801	CAC	» C»	810
												TTC					
С	Р		P	Е	G	G	L	K	Ι	A	A	F	N	I	Q	Т	F
GGG	GAG	819 ACC	AAG	ATG	828 TCC	AAT	GCC	837 ACC	CTC	GTC	846 AGC	TAC	ATT	855 GTG	CAG	ATC	864 CTG
G	Е	т	K	M	S	N	A	т	L	v	S	Y	I	V	Q	I	L
AGC	CGC	873 TAC	GAC	ATC	882 GCC		GTC			GTC		GAC	AGC	909 CAC		ACT	918 GCC
 S	 R	Y	-		 A	 L	v	Q	 E	v	 R	D	 S	Н	 L	т	Α
CTC		927		CTC	936		ርጥር	945 ' AAT		GA(954 CCA		GAC	963		CAC	972 TAC
 V	 G	 K	L	L	D	 N	 L	 N	 Q	D	 A	 P	 D	т	Y		Y
V	G	981		n	990			999		D	1008		_	1017			1026
GTO	G GT			G CCA			CGG									TT(GTG
V	V	S	E	Р	L	G	R	N	S	Y	K	E	R	Y	L	F	V
TAC			r ga	C CA		G TC	r GC	G GT	G GAG	C AG	C TAG		AT C	C GA'	r GA	r gg	1080 C TGC
 Y																	C
GA	G CC	108 C TG	-	g aa			C TT				111 .G CC		C AT				1134 C TTC
 E																	 F
																	1188
																	C CCG
S	. I	₹ F	, J	E	: v	R	E	F	A	.)	V	у Р	L	H	I A	. A	Y P
		119	97		120	16		121	5		122	24		123	3		1242

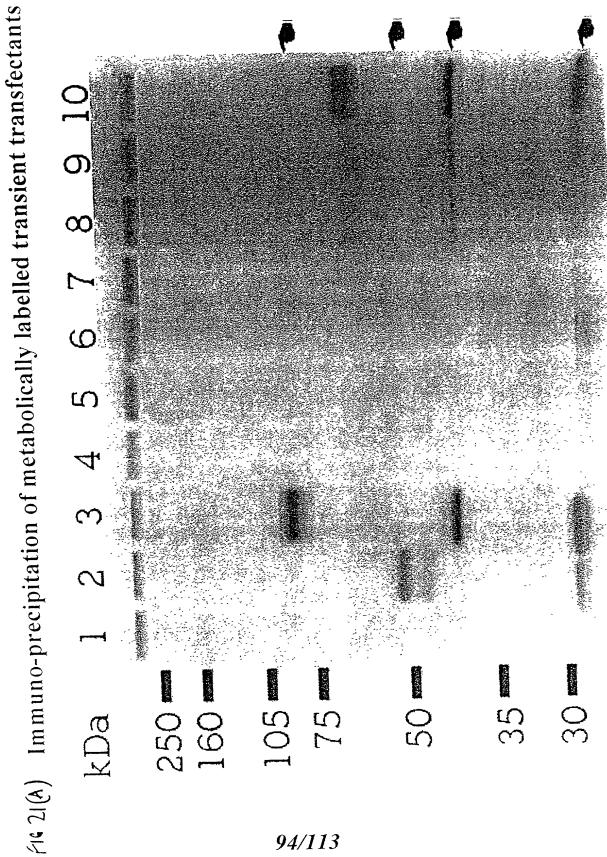
GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA --- --- --- --- --- --- --- --- --- --- --- --- ---1251 1260 1269 1278 1287 1296 GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC EKWGLEDVMLMGDFNAGC 1305 1314 1323 1332 1341 1350 AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC --- --- --- --- --- --- --- --- --- --- --- --- --- ---1359 1368 1377 1386 1395 1404 TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT --- --- --- --- --- --- --- --- --- --- --- --- --- $\begin{smallmatrix} F&Q&W&L&I&P&D&S&A&D&T&T&A&T&P&T&H&C \end{smallmatrix}$ 1449 1458 1413 1422 1431 1440 GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC --- --- --- --- --- --- --- --- --- --- --- --- ---1467 1476 1485 1494 1503 1512 GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG D S A L P F N F Q A A Y G L S D Q L 1530 1539 1548 1557 1566 1521 GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA --- --- --- --- --- --- --- --- --- --- --- --- ---A Q A I S D H Y P V E V M L K G G G 1575 1584 CCC AAA AAG AAG CGC AAG GTT TGA 3' ___ --- --- --- --- ---

P K K K R K V *

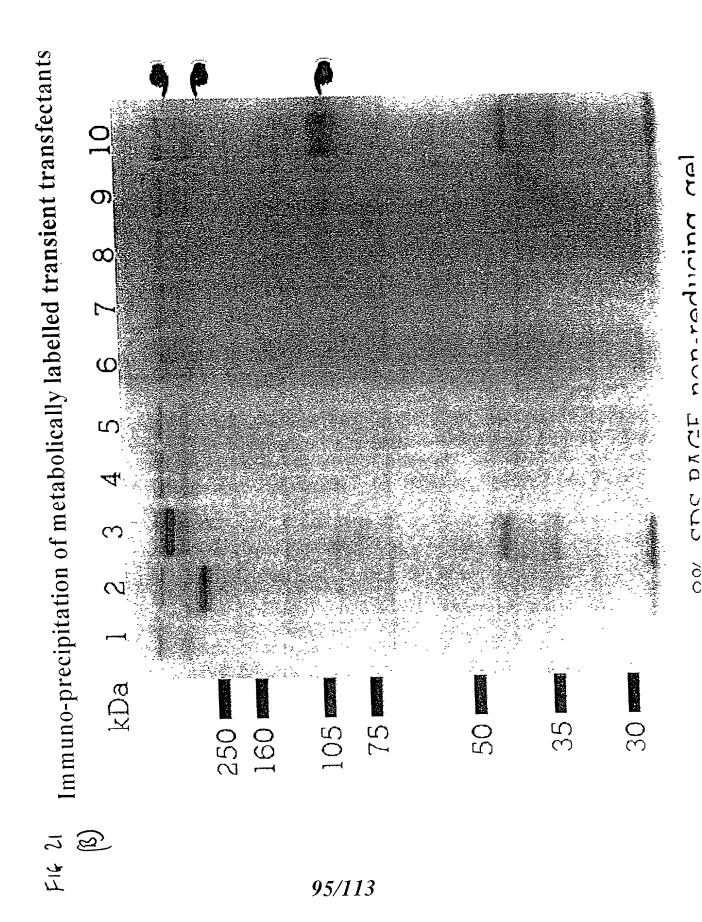
F19 20

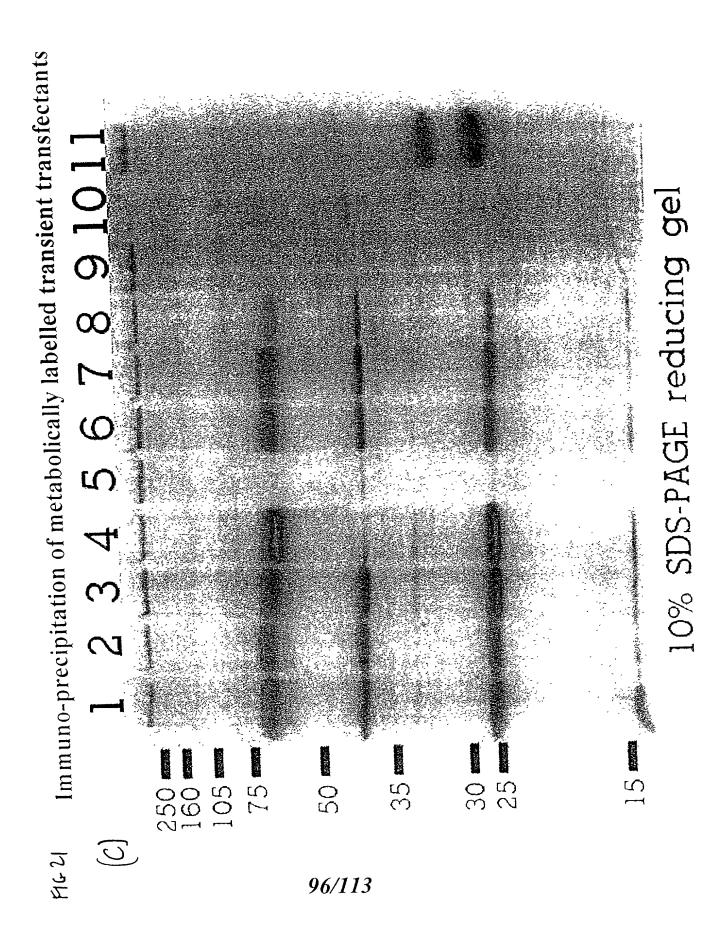
Mammalian expression of humanised HMFG1-DNase constructs

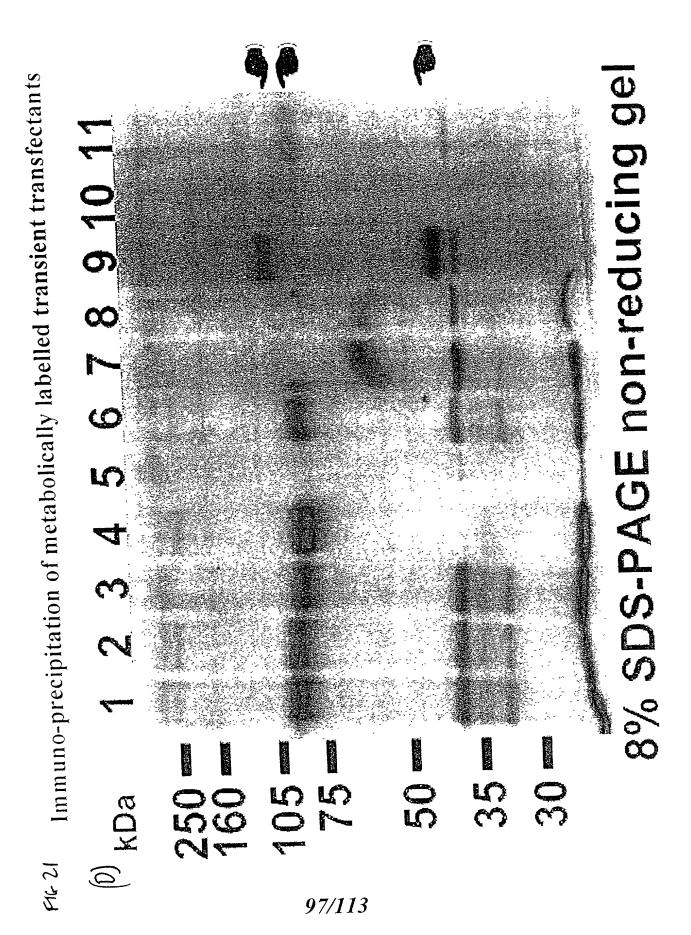
le term:



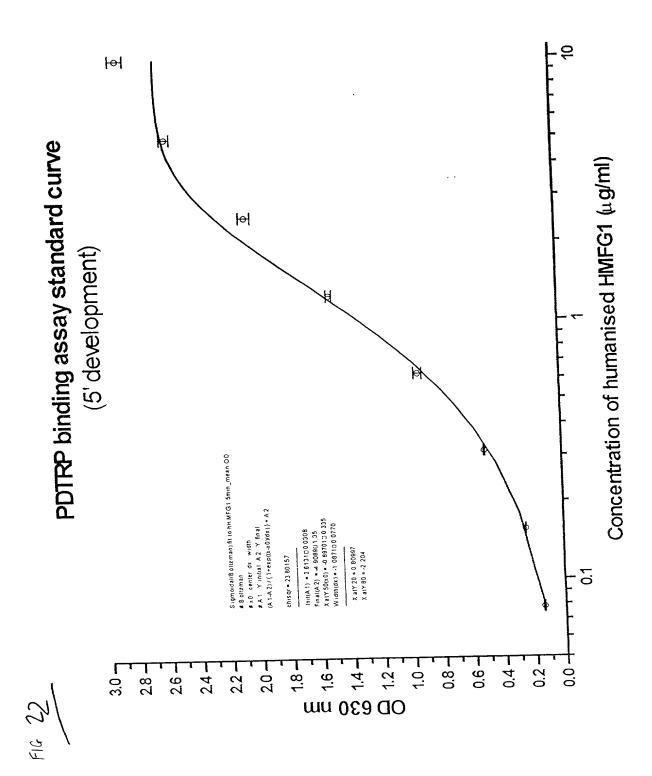
8% SDS-PAGE reducing gel







:



Corrected bovine DNase I standard curves at various time points

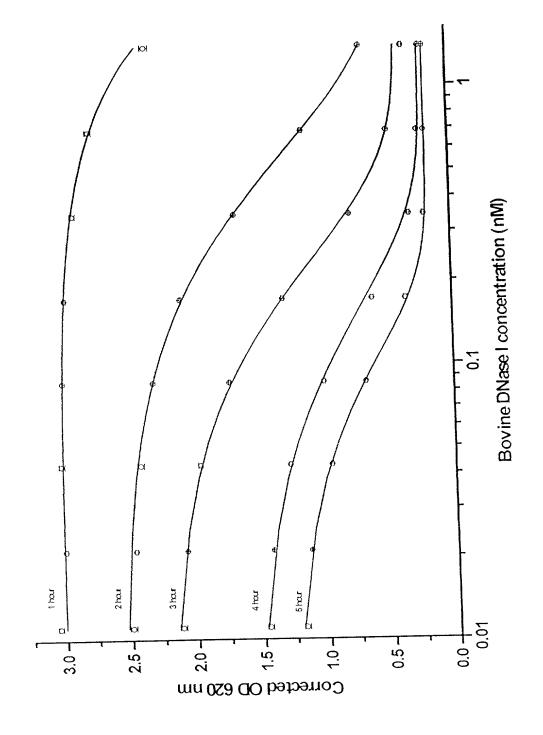
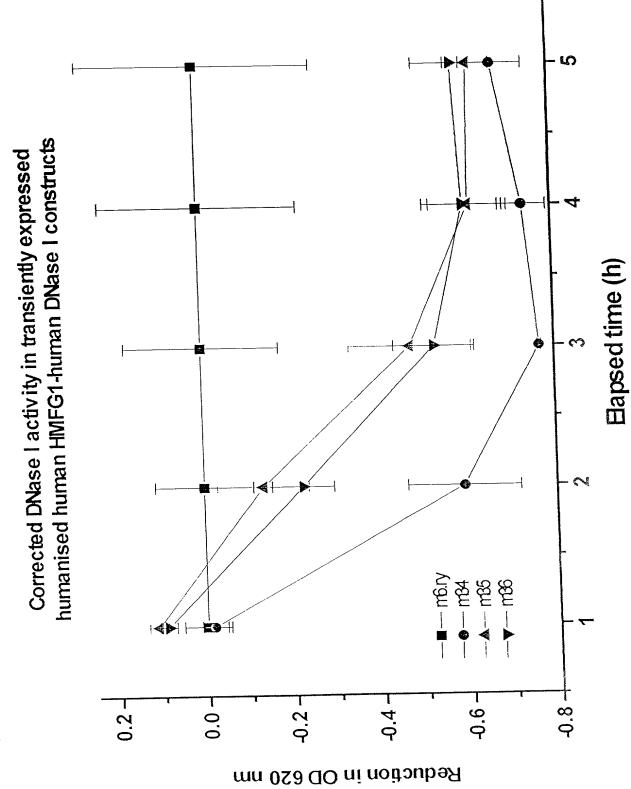
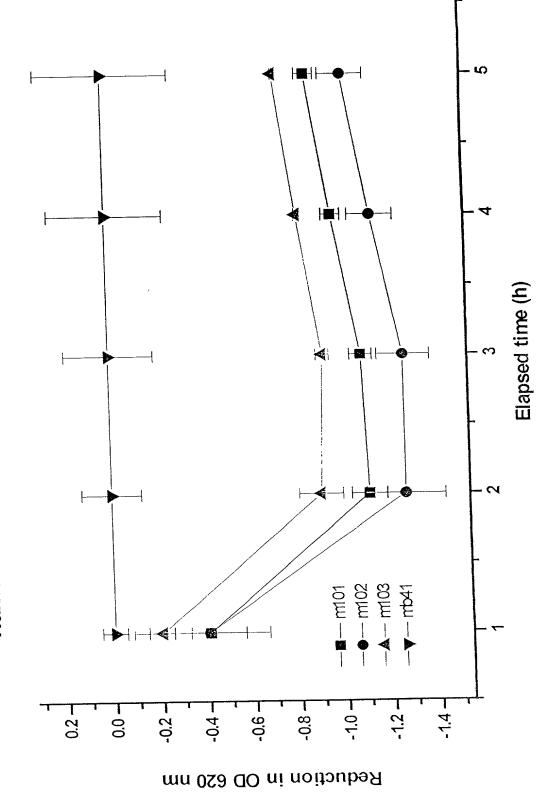


FIG 23

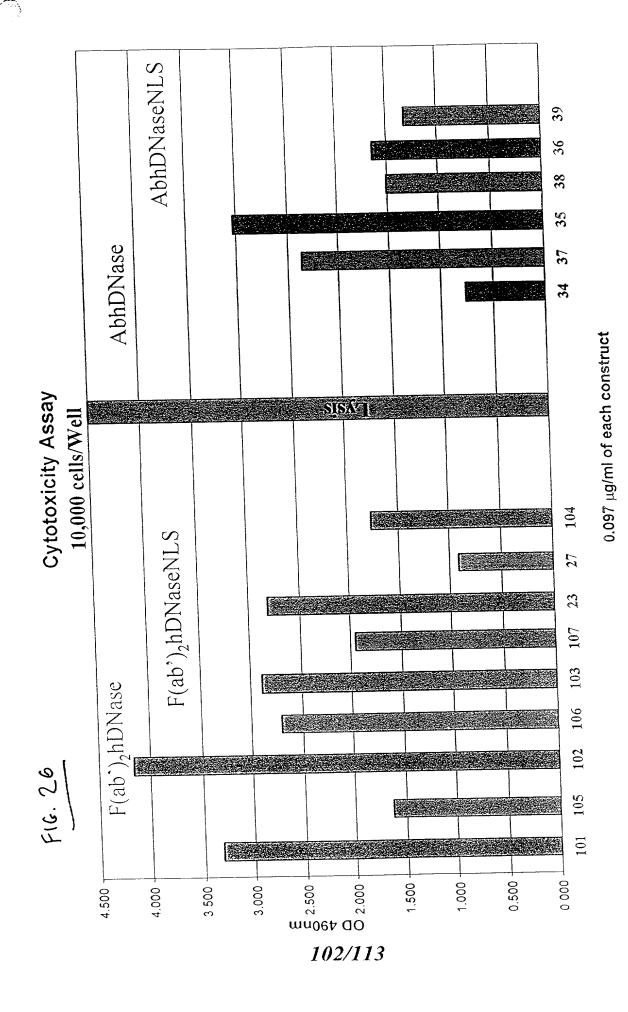
100/113



Corrected DNase I activity in transiently expressed humanised HMFG1 F(ab')2-human DNase I fusions



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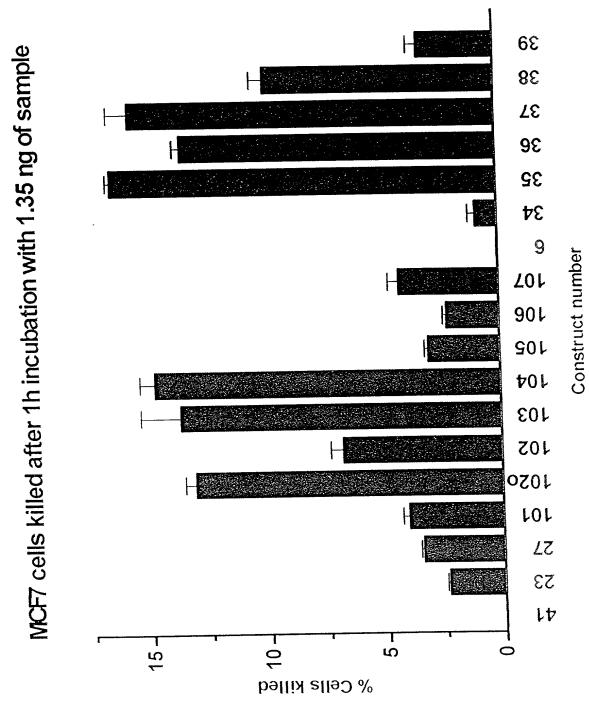
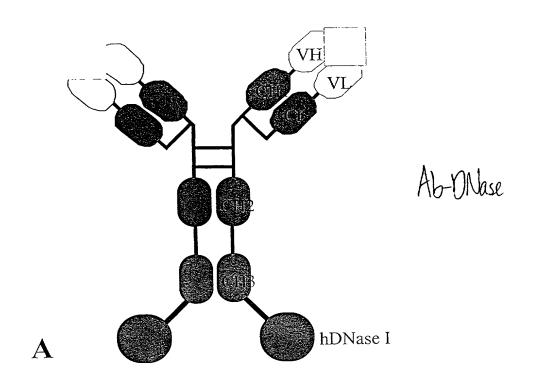


FIG 27

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Figure 28



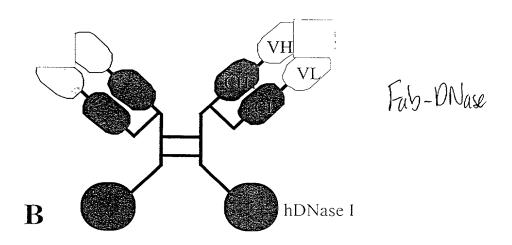
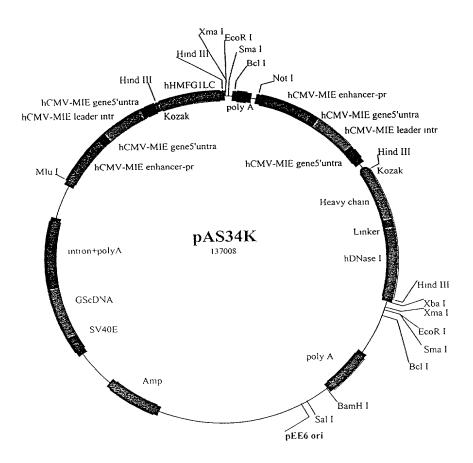
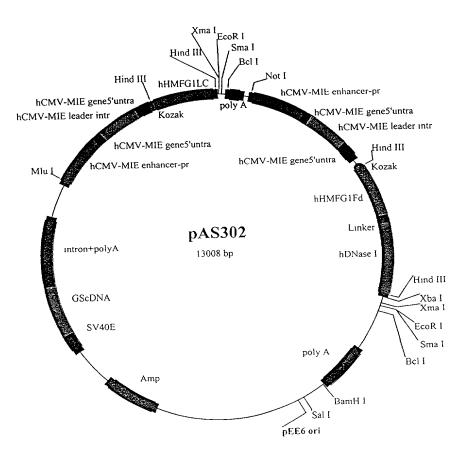


Figure 29



Ab-DNase

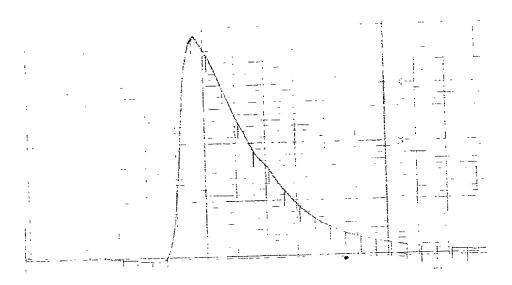
Figure 30



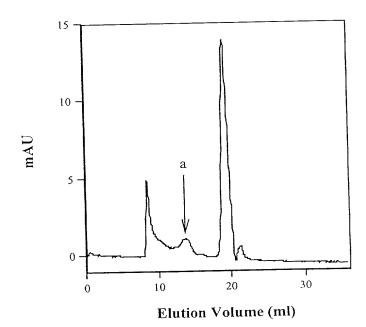
Fab-DNase

Figure 31

A



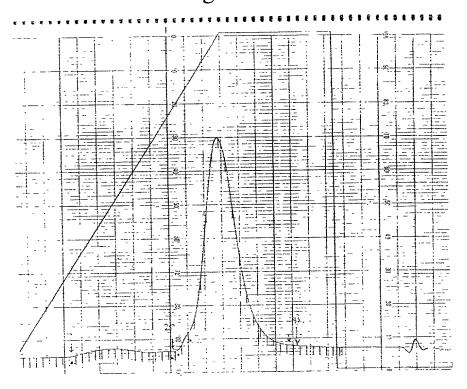
B



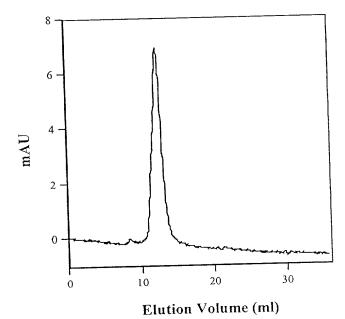
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Figure 32



B



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Figure 33

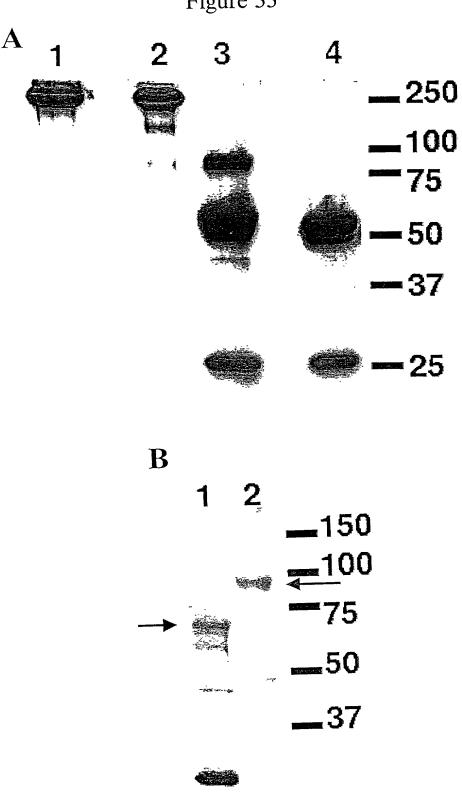
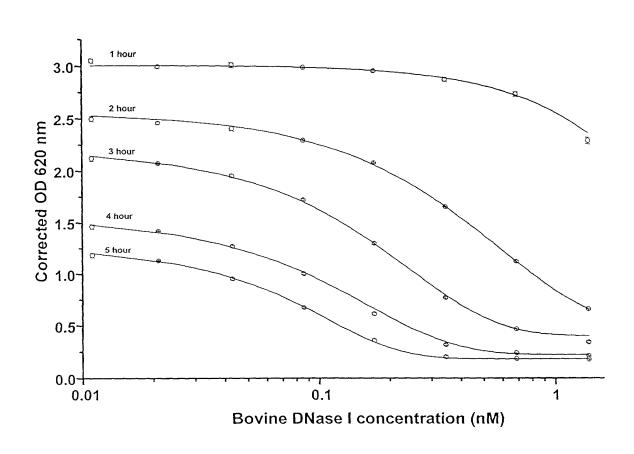


Figure 34

Bovine DNase I standard curves at various time points



 ${\bf A}$

Figure 34 – cont.



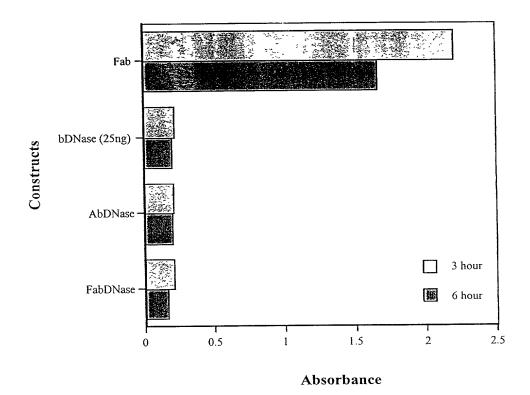


Figure 35

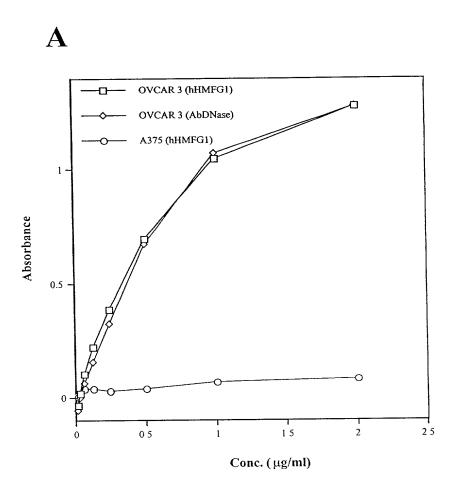


Figure 35 – cont.

B

